

FORM PTO-1390
(REV. 12-29-99)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

66040-9651

TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 371

U.S. APPLICATION NO. (if known, see 37 CFR 1.5)

09/530663

INTERNATIONAL APPLICATION NO.
PCT/US98/24138INTERNATIONAL FILING DATE
12 November 1998PRIORITY DATE CLAIMED
12 November 1997

TITLE OF INVENTION GENETIC ENGINEERING OF LIGNIN BIOSYNTHESIS IN PLANTS

APPLICANT(S) FOR DO/EO/US Vincent Lee C. Chiang; Chung-Jui Tsai; Wen-Jing Hu

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☐ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ has been transmitted by the International Bureau.
 - c. ☒ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☐ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☐ A **FIRST** preliminary amendment.
☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information:

Small Entity Declaration

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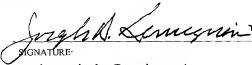
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| U.S. APPLICATION NO. 09/530663 INTERNATIONAL APPLICATION NO. PCT/US98/24138 | | ATTORNEY'S DOCKET NUMBER 66040-9651 | |
| 17. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO \$970.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$840.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$690.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4) \$670.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4) \$96.00 | | CALCULATIONS PTO USE ONLY | |
| ENTER APPROPRIATE BASIC FEE AMOUNT = | | \$ 96.00 | |
| Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)). | | \$ | |
| # CLAIMS | NUMBER FILED | NUMBER EXTRA | RATE |
| Total claims | 53 - 20 = | 33 | X \$18.00 |
| Independent claims | 16 - 3 = | 13 | X \$78.00 |
| MULTIPLE DEPENDENT CLAIM(S) (if applicable) | | | + \$260.00 |
| TOTAL OF ABOVE CALCULATIONS = | | \$ 1704.00 | |
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| SEND ALL CORRESPONDENCE TO Joseph A. Gemignani Michael Best & Friedrich LLP 100 East Wisconsin Avenue Milwaukee, WI 53202 | | | |
| | |  SIGNATURE: Joseph A. Gemignani | |
| | | NAME 19,482 | |
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**STATEMENT CLAIMING SMALL ENTITY STATUS
37 CFR 1.8(f) & 1.27(d) - NONPROFIT ORGANIZATION**

Document Number (Optional)
86040-9651

Applicant, Patentee, or Identifier: Chiang, et al.
Application or Patent No.: PCT/US98/24138
Filed or Issued: November 12, 1998
Title: GENETIC ENGINEERING OF LIGNIN BIOSYNTHESIS IN PLANTS

I hereby state that I am an official empowered to act on behalf of the nonprofit organization identified below.
NAME OF NONPROFIT ORGANIZATION: Board of Control of Michigan Technological University
ADDRESS OF NONPROFIT ORGANIZATION: 1400 Townsend Drive, Houghton, MI 49931

TYPE OF NONPROFIT ORGANIZATION:

- ☒ UNIVERSITY OR OTHER INSTITUTION OF HIGHER EDUCATION
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I hereby state that the nonprofit organization identified above qualifies as a nonprofit organization as defined in 37 CFR 1.8(a) for purposes of paying reduced fees to the United States Patent and Trademark Office regarding the invention described in:

- ☐ the specification filed herewith with title as listed above.
- ☒ the application identified above.
- ☐ the patent identified above.

I hereby state that rights under contract or law have been conveyed to and remain with the nonprofit organization regarding the above identified invention. If the rights held by the nonprofit organization are not exclusive, each individual, concern, or organization having rights in the invention must file separate statements as to their status as small entities and that no rights to the invention are held by any person, other than the inventor, who would not qualify as an independent inventor under 37 CFR 1.8(c) if that person made the invention, or by any concern which would not qualify as a small business concern under 37 CFR 1.8(d) or a nonprofit organization under 37 CFR 1.8(e).

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NAME OF PERSON SIGNING: William J. McGarry
TITLE IN ORGANIZATION OF PERSON SIGNING: Treasurer, Board of Control
ADDRESS OF PERSON SIGNING: 1400 Townsend Drive, Houghton, Michigan 49931
SIGNATURE: William J. McGarry DATE: 3 May 00

05230837-07100

GENETIC ENGINEERING OF LIGNIN BIOSYNTHESIS IN PLANTS

5 Cross-Reference to Related Applications

This is a continuation-in-part of U.S. application Serial No. 08/969,046, filed November 12, 1997, the disclosure of which is incorporated by reference herein.

Field of the Invention

- 10 The invention relates to genetically modifying plants, e.g., trees, through manipulation of the lignin biosynthesis pathway, and more particularly, to genetically modifying plants through the down regulation of 4-coumarate Co-enzyme A ligase (4CL) to achieve faster growth. Down regulation of 4CL may also achieve altered lignin content, and/or altered lignin structure, and/or altered
- 15 cellulose content, and/or altered disease resistance of the trees. Moreover, promoters of the 4CL genes are useful to drive gene expression specifically in xylem tissue or specifically in epidermal tissues.

Background of the Invention

- Genetic engineering of plants to conform to desired traits has shifted the
- 20 emphasis in plant improvement away from the traditional breeding programs during the past decade. Although research on genetic engineering of plants has been vigorous, the progress has been slow.

- The ability to make plants grow faster continues to be the top objective of many companies worldwide. The ability to genetically increase the optimal
- 25 growth of plants would be a commercially significant improvement. Faster growing plants could be used by all sectors of the agriculture and forest products industries worldwide.

- Lignin, a complex phenolic polymer, is a major component in cell walls of secondary xylem. In general, lignin constitutes 25% of the dry weight of the
- 30 wood, making it the second most abundant organic compound on earth after cellulose. Although lignin plays an important role in plants, it usually represents an obstacle to utilizing biomass in several applications. For example, in wood

pulp production, lignin has to be removed through expensive and polluting processes in order to recover cellulose.

Thus, it is desirable to genetically engineer plants with reduced lignin content and/or altered lignin composition that can be utilized more efficiently.

- 5 Plants that could be genetically engineered with a reduced amount of lignin would be commercially valuable. These genetically engineered plants would be less expensive to pulp because, in essence, part of the pulping has already been performed due to the reduced amount of lignin. Further, plants with increased cellulose content would also be commercially valuable to the pulp and paper
- 10 industry.

Disease resistance in plants is also a desirable plant trait. The impact of disease resistance in plants on the economy of plant products industry worldwide is significant.

- Thus, what is needed is the identification and characterization of genes
- 15 useful to enhance plant growth, alter lignin content and/or structure in plants, alter cellulose content in plants, and/or provide or enhance disease resistance of plants.

Summary of the Invention

- The invention provides a method to genetically alter plants through the
- 20 down regulation (decrease) or inhibition of native (endogenous) 4-coumarate Co-enzyme A ligase (4CL) in that plant. Such down regulation of 4-coumarate Co-enzyme A ligase results in faster growth, and/or reduced lignin content, and/or altered lignin structure, and/or altered cellulose content, and/or altered disease resistance in the genetically altered plant. The invention also provides
- 25 for genetically engineered plants, e.g., transformed or transgenic plants, which have been altered to down regulate or inhibit native 4-coumarate Co-enzyme A ligase in the plant so as to achieve faster growth, and/or reduced lignin content, and/or altered lignin structure, and/or increased cellulose content, and/or increased disease resistance. Preferred genetically altered plants include trees,
- 30 e.g., angiosperms or gymnosperms, forage crops, and more preferably a forest tree, e.g., Populus. Preferred angiosperms include, but are not limited to, Populus, Acacia, Sweetgum, yellow poplar, maple and birch, including pure

lines and hybrids thereof. Preferred gymnosperms include, but are not limited to, Pine, Spruce, Douglas-fir and hemlock.

The invention further provides a transgenic plant, the genome of which is augmented by a recombinant DNA molecule encoding 4-coumarate Co-enzyme A ligase, or a recombinant DNA molecule comprising an antisense 4-coumarate Co-enzyme A ligase gene, or a fragment thereof. The recombinant DNA molecule is expressed so as to down regulate, decrease or inhibit lignin pathway 4-coumarate Co-enzyme A ligase.

The invention also provides an isolated and purified DNA molecule comprising a DNA segment comprising a transcriptional regulatory control region of a 4-coumarate Co-enzyme A ligase gene. Preferably, the transcriptional regulatory region comprises a promoter. Tissue specific promoters of a 4-coumarate Co-enzyme A ligase gene can be used to manipulate gene expression in target tissue such as xylem and epidermal tissues, as described hereinbelow. Preferably, the promoter is derived from aspen DNA. Therefore, the invention also provides an expression cassette comprising a transcriptional regulatory region of a 4-coumarate co-enzyme A ligase gene, a method of using the region to express a preselected DNA segment in a tissue-specific manner in plant cells, and a transgenic plant comprising the expression cassette.

Also provided is a method to alter, e.g., enhance, plant growth. The method comprises introducing an expression cassette into cells of a plant, e.g., the cells of a tree, so as to yield genetically altered plant cells. The expression cassette comprises a recombinant DNA molecule, segment, or sequence, comprising a 4-coumarate Co-enzyme A ligase gene, or a fragment thereof. Preferably, the 4-coumarate Co-enzyme A ligase gene, or fragment thereof, is in antisense orientation. The 4-coumarate Co-enzyme A ligase gene may be a homologous or heterologous 4-coumarate Co-enzyme A ligase gene. The transformed plant cells are regenerated to provide a genetically altered, e.g., transgenic, plant. The recombinant DNA is expressed in the cells of the regenerated, genetically altered plant in an amount that confers enhanced or accelerated growth to the regenerated, genetically altered plant relative to the

corresponding non-genetically altered plant. Preferably, the genetically altered plant is a tree. It is preferred that a genetically altered tree of the invention has an increase in height, leaf size, diameter and/or average internode length relative to the corresponding non-genetically altered tree.

- 5 Hence, the invention also provides for a genetically altered plant, the genome of which is augmented by a recombinant DNA molecule encoding 4-coumarate Co-enzyme A ligase, or a recombinant DNA molecule comprising an antisense 4-coumarate Co-enzyme A ligase gene, or fragment thereof, which plant has altered growth characteristics relative to the corresponding non-
10 genetically altered plant.

- Further provided is a method to genetically alter plants so as to change or alter their lignin structure. The method comprises introducing an expression cassette into cells of a plant, e.g., a tree, so as to yield genetically altered plant cells. The expression cassette preferably comprises an antisense recombinant
15 DNA molecule, segment or sequence comprising a 4-coumarate Co-enzyme A ligase gene, or a fragment thereof. The transformed plant cells are regenerated to provide a regenerated, genetically altered plant. The recombinant DNA is expressed in the cells of the regenerated, genetically altered plant in an amount that alters the lignin structure in the cells of the plant relative to the
20 corresponding non-genetically altered plant.

- Also provided is a method for altering the lignin content in a plant. The method comprises introducing an expression cassette comprising a recombinant DNA molecule comprising a 4-coumarate Co-enzyme A ligase gene operably linked to a promoter functional in a plant cell into the cells of a plant. The plant
25 cells are regenerated so as to yield a genetically altered plant. The recombinant DNA molecule is expressed in the cells of the regenerated plant in an amount effective to alter the lignin content in the plant cells. Preferably, the lignin content is reduced. Also preferably, the lignin content is reduced in a tissue-specific manner. In particular, a reduction in lignin content in forage crops is
30 useful as the digestability of these crops by ruminants is increased. Also preferably, the 4-coumarate Co-enzyme A ligase gene is in an antisense orientation relative to the promoter.

Further provided is a genetically altered, e.g., transgenic, plant having an altered lignin content in the plant cells. The plant comprises a recombinant DNA molecule comprising a nucleotide sequence encoding a plant 4-coumarate Co-enzyme A ligase operably linked to a promoter so that the recombinant DNA molecule is expressed in an amount effective to alter the lignin content of the plant.

Yet another embodiment of the invention is a method to alter, e.g., increase, the cellulose content in plants. The method comprises introducing an expression cassette into cells of a plant, e.g., a tree, so as to yield genetically altered plant cells. The expression cassette preferably comprises an antisense recombinant DNA molecule, segment or sequence comprising a 4-coumarate Co-enzyme A ligase gene, or a fragment thereof, operably linked to a promoter functional in a plant cell. The transformed plant cells are regenerated to provide a regenerated, genetically altered plant. The recombinant DNA is expressed in the cells of the regenerated, genetically altered plant in an amount that alters the cellulose content in plant. Thus, the invention further provides a genetically altered, e.g., transgenic, plant having an altered cellulose content.

The invention also provides a method to genetically alter plants to increase their disease resistance, e.g., to fungal pathogens. The method comprises introducing an expression cassette comprising a recombinant DNA molecule comprising a nucleotide sequence encoding a 4-coumarate Co-enzyme A ligase operably linked to a promoter functional in a plant cell into cells of a plant. The transformed plant cells are regenerated to provide a genetically altered plant. The recombinant DNA molecule is expressed in the cells of the regenerated, genetically altered plant in an amount effective to render the plant resistant to disease. Preferably, the recombinant DNA molecule is expressed in amount that decreases the amount of lignin in the plant and/or increases the amount of phenolic compounds which are toxic to fungal pathogens. Hence, the invention also provides a transgenic plant, which is substantially resistant to disease. The plant comprises a native 4-coumarate Co-enzyme A ligase gene, and a recombinant DNA molecule comprising a nucleotide sequence encoding 4-coumarate Co-enzyme A ligase operably linked to a promoter functional in a

plant wherein the recombinant DNA molecule is expressed in an amount effective to confer resistance to the transgenic plant.

Other features and advantages of the invention will become apparent to those of ordinary skill in the art upon review of the following drawings, detailed description and claims.

Brief Description of the Drawings

Fig. 1 is a schematic of a phenylpropanoid pathway;

Fig. 2 is a diagram of Agrobacterium T-DNA gene construct pA4CL1;

Fig. 3 is a restriction map of genomic clone Pt4CL1g-4;

Fig. 4 is a restriction map of genomic clone Pt4CL2g-11;

Fig. 5 is a restriction map of subcloned pT4CL1 gene promoter p7Z-4XS;

Fig. 6 is a restriction map of subcloned pT4CL2 gene promoter pSK-11HE;

Fig. 7 is an Agrobacterium T-DNA construct of Pt4CL1 promoter and

GUS fusion gene Pt4CL1p-GUS; and

Fig. 8 is an Agrobacterium T-DNA construct of Pt4CL2 promoter and GUS fusion gene, Pt4CL2p-GUS.

Fig. 9 shows biosynthetic pathways to guaiacyl (coniferyl alcohol **9a**) and syringyl (sinapyl alcohol **9b**) monolignols for the formation of guaiacyl-syringyl

lignin in wood angiosperms. Enzymes are indicated for each reaction step.

C4H, cinnamic acid 4-hydroxylase; C3H, 4-coumaric acid 3-hydroxylase; COMT, caffeic acid *O*-methyltransferase; F5H, ferulic acid 5-hydroxylase; CCR, cinnamoyl-CoA reductase; CAD, cinnamyl alcohol dehydrogenase. Aspen 4CL (Pt4CL1) converts 4-coumaric **2**, caffeic **3**, ferulic **4**, 5-hydroxyferulic **5**, and sinapic **6** acids into their corresponding thioesters for the formation of feruloyl-CoA **7a** and sinapoyl-CoA **7b**, leading to **9a** and **9b**, respectively.

Fig. 10. The effects of down-regulation of Pt4CL1 expression on Pt4CL1 activity and lignin accumulation in transgenic aspen. (A) Northern blot analysis of Pt4CL1 transcript levels in control (lane C) and transgenic aspen (3, 4, 5, 6, 8, and 9). Each lane contained 20 µg of total RNA extracted from developing xylem and the blot was hybridized (Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, NY (1989)) with

Pt4CL1 cDNA. (B) Pt4CL1 enzyme activities in developing xylem tissues. Crude protein (40 μ g) extracted from xylem tissue was assayed spectrophotometrically for Pt4CL1 activities with various hydroxylated cinnamic acids (Ranjewa et al., 1976). Error bars represent SD values of three replicates.

(C) Levels of lignin reduction in woody stem of transgenic lines as compared to the control, based on the lignin contents presented in Table 7. (D and E) Fluorescence microscopy showing transverse sections of the 20th internode from control (D) and transgenic line 6 (E). Lignin autofluorescence was visualized following UV-excitation at 365 nm.

- Fig. 11 depicts regions of the HSQC spectra (NMR experiments were performed at 360 MHz on a Bruker DRX-360 using a narrow bore probe with inverse coil geometry (proton coils closest to the sample) and with gradients. Experiments used were standard Bruker implementations of gradient-selected inverse (¹H-detected) HSQC (Palmer et al., J. Magn. Reson. Ser. A, 111, 70 (1991)), HSQC-TOCSY (Braunschweiler et al., J. Magn. Reson., 53, 521 (1983)), and HMQC (Ruiz-Cabello et al., J. Magn. Reson., 100, 282 (1992)) along with the standard 1D ¹³C (proton-decoupled) and ¹H NMR experiments. TOCSY experiments used a 100 ms spin lock period; HMBC used either an 80 or a 100 ms long-range coupling delay.) of isolated milled wood lignins from (A) control and (B) transgenic line 6. Structure assignments (Ralph et al., 1997) reveal the existence of some major structural units in both samples that are common to angiosperm lignin. The *erythro*-($\delta_{\text{C}_\alpha}/\delta_{\text{H}_\alpha}$:75.4/6.05) and *threo*-($\delta_{\text{C}_\alpha}/\delta_{\text{H}_\alpha}$:76.6/6.08) isomers of β -aryl ethers 10 are indicated. 5-5-Homo-coupling of coniferyl alcohol 9a involved in dibenzodioxocins 13 ($\delta_{\text{C}_\alpha}/\delta_{\text{H}_\alpha}$:85.3/4.94) (Ralph et al., 1997) was not detected in either sample. Yellow contours are from intense methoxyl signals and light green contours form xylan residues. Other components (gray contours) in both lignin samples, not relevant or not identified, are commonly seen in many other angiosperm lignin preparations.

- Fig. 12 shows enhanced growth in transgenic aspen. (A) 10-Week-old plants of control and four transgenic aspen grown in a greenhouse (ruler = 25 cm). (B) Control and transgenic leaves from the 10th internodes. (C to F) SE images of stem transverse sections of control [C (bar = 50 μ m) and E (bar = 10

- μm)] and transgenic line 6 [D (bar = 50 μm) and F (bar = 10 μm)]. (G) 2-week-old *ex vitro* rooted stem cuttings from control and transgenic aspen lines 5 and 6. Two cuttings from each line are shown. (H) Leaf upper epidermal cell area. Values represent the mean of at least 100 determinations per leaf. Sample SD was 15 to 20% of the mean for all determinations.

- Before one embodiment of the invention is explained in detail, it is to be understood that the invention is not limited in its application to the details set forth in the following description of the preferred embodiment. The invention is capable of other embodiments and of being practiced or being carried out in various ways. Also, it is to be understood that the phraseology and terminology used herein is for the purpose of description and should not be regarded as limiting.

Detailed Description of the Invention

- The invention pertains to genetically down regulating a lignin pathway 4-coumarate Co-enzyme A ligase (4CL) in a plant. Plants which have been genetically transformed to down regulate 4CL will hereafter be called transgenic plants. Such down regulation can result in faster growing plants. Such down regulation can also result in a reduction in the lignin content of the plants and/or altered lignin structure. Such down regulation can further result in increased cellulose content. Such down regulation may also result in increased disease resistance. Further, by using a specific 4CL promoter, targeted tissue-specific gene expression can be achieved in either the xylem or the epidermal tissues of the plant.

A. 4CL

- Lignin is synthesized by the oxidative coupling of three monolignols (coumaryl, coniferyl and sinapyl alcohols) formed via the phenylpropanoid pathway as shown in Fig. 1. Reactions in the phenylpropanoid pathway include the deamination of phenylalanine to cinnamic acid followed by hydroxylations, methylations and activation of substituted cinnamic acids to coenzyme A (CoA) esters. The CoA esters are then reduced to form monolignols which are secreted from cells to form lignin.

The products of the phenylpropanoid pathway are not only required for the synthesis of lignin but also required for the synthesis of a wide range of aromatic compounds including flavonoids, phytoalexins, stilbenes and suberin.

- In the phenylpropanoid pathway, 4CL activates a number of cinnamic acid derivatives, including 4-coumaric acid, caffeic acid, ferulic acid, 5-hydroxyferulic acid and sinapic acid. The resulting products, CoA esters, serve as substrates for entry into various branch pathways, such as lignin, flavonoids, phytoalexins, stilbenes and suberin. The esterification reactions catalyzed by 4CL require high energy and the reactions are not likely to occur without 4CL.
- 4CL is important in making a continuous flow of the lignin biosynthesis pathway. 4CL is also important because it is located at the branching points of the phenylpropanoid metabolism. 4CL is suggested to play a pivotal role in regulating carbon flow into specific branch pathways of the phenylpropanoid metabolism in response to stages of development and environmental stress.
- The basic properties of 4CL are quite uniform. 4CL depends on ATP as a cosubstrate and requires Mg^{2+} as a cofactor. The optimal pH for 4CL ranges from pH 7.0 to 8.5 and the molecular weight of 4CL isoforms from various plant species ranges from 40 kD to 75 kD. Most 4CLs have high affinity for substituted cinnamic acids. 4CL has the highest activity with 4-coumaric acid.
- 4CL cDNA sequences have been reported for parsley, potato, soybean, rice, loblolly pine, *Arabidopsis*, *Lithospermum*, *Vanilla* and tobacco. 4CL genes have been isolated and sequenced for parsley, rice, potato and loblolly pine. The analysis of 4CL cDNAs and genes indicates that 4CL is encoded by multiple/divergent genes in rice, soybean, and *Lithospermum*, very similar genes in parsley, potato, tobacco, and loblolly pine, and a single gene in *Arabidopsis*.
- Two similar 4CL cDNAs in parsley, potato and tobacco have been shown to be expressed at similar level in response to environmental stress and during different developmental stages. Two distinct 4CL cDNAs in soybean and *Lithospermum* have shown different expression levels when pathogens or chemicals were applied to the cell cultures. It appears that the expression of the 4CL genes is developmentally regulated and inducible by many environmental

stresses at the transcription level. 4CL promoters have been isolated and sequenced for parsley, rice and potato.

Alignment of deduced amino acid sequences of cloned plant 4CL sequences reveals two highly conserved regions. The first conserved region (LPYSSGTTGLPK; SEQ ID NO:7), proposed to designate a putative AMP-binding region, consists of a serine/threonine/glycine-rich domain followed by a proline/lysine glycine triplet. The second conserved region (GEICIRG; SEQ ID NO:8) contains one common Cys residue. The amino acid sequences of 4CL from plants contain a total of five conserved Cys residues.

The description of the invention hereafter refers to the tree species aspen, and in particular quaking aspen (*Populus tremuloides* Michx), when necessary for the sake of example. However, it should be noted that the invention is not limited to genetic transformation of trees such as aspen. The method of the present invention is capable of being practiced for other plant species, including for example, other angiosperm, and other gymnosperm forest plants species, legumes, grasses, other forage crops and the like.

Preferably, the 4CL down regulation is accomplished through transformation with a homologous 4CL sequence in an antisense orientation. However, it should be noted that a heterologous antisense 4CL sequence could be utilized and incorporated into a plant species to down regulate 4CL if the heterologous 4CL gene sequence has a high nucleotide sequence homology or identity of at least about 70%, more preferably at least about 80%, and more preferably at least about 90%, to the endogenous (native) 4CL gene sequence of that plant species, e.g., a tree species.

In addition, plants transformed with a sense 4CL sequence may also cause a sequence homology-based cosuppression of the expression of the transgene and endogenous 4CL gene, thereby achieving down regulation of 4CL in these plants.

B. Isolation of 4CL cDNAs

The present invention utilizes a homologous 4CL sequence to genetically alter plants. The example described below utilizes a cDNA clone of the quaking aspen 4CL gene to genetically alter quaking aspen.

Two 4CL cDNAs, Pt4CL1 and Pt4CL2, have been isolated from quaking aspen. Pt4CL1 cDNA is lignin pathway-specific and is different from Pt4CL2 cDNA, which is involved in flavonoid synthesis. It should be noted that the methods described below are set forth as an example and should not be considered limiting. The sequences of these 4CL cDNA clones are available from Genbank, Accession Nos. AF041049 and AF041050.

Pt4CL1 and Pt4CL2 genomic clones including their 5' -end regulatory promoter sequences were also isolated. The promotor of Pt4CL 1 (Pt4CL1p) directs xylem tissue-specific gene expression in a plant, whereas the promoter of Pt4CL2 (Pt4CL2p) drives the expression of genes specifically in epidermal tissues of stem and leaf of a plant. These tissue specific promoters will be discussed in more length below.

Young leaves and shoot tips are collected from greenhouse-grown quaking aspen (*Populus tremuloides* Michx). Differentiating xylem is collected from three to four year old quaking aspen. The bark is peeled from the tree exposing the developing secondary xylem on the woody stem. Developing secondary xylem is scraped from the stem and bark with a razor blade and immediately frozen in liquid nitrogen until use.

Total RNA is isolated from the young leaves, shoot tips, and xylem following the method of Bugos et al., Biotechniques 19(5):734-737 (1995). Poly(A)⁺ RNA is purified from total RNA using Poly(A)⁺ mRNA Isolation Kit from Tel-test B, Inc. A unidirectional Lambda gt22 expression cDNA library was constructed from the xylem mRNA using Superscript λ System from Life Technologies, Inc. and Gigapack Packaging Extracts from Stratagene. The Pt4CL1 cDNA was obtained by screening the cDNA library with a ³²P-labeled parsley 4CL cDNA probe. The parsley 4CL cDNA (pc4CL2) has Genbank Accession No. X13325.

The Pt4CL2 cDNA was obtained by RT-PCR. The reverse transcription of total RNA isolated from shoot tips was carried out using the Superscript II reverse transcriptase from Life Technologies. Two sense primers (R1S, 5'-TTGGATCCGGIACIACIGGIYTICCIAARGG-3'; SEQ ID NO:9 and H1S, 5'-TTGGATCCGTIGCICARCARGTIGAYGG-3'; SEQ ID NO:10) were designed

around the first consensus AMP-binding region of 4CL that was previously discussed. One antisense primer (R2A, 5'-ATGTCGACCICKDATRCADATYTCICC-3'; SEQ ID NO:11) was designed based on the sequence of the putative catalytic motif GEICIRG (SEQ ID NO:12).

- 5 One fifth of the reverse transcription reaction (4 μ l) is used as the template in a 50 μ l PCR reaction containing 1X reaction buffer, 200 μ M each deoxyribonucleotide triphosphate, 2 μ M each R1S and oligo-dT (20 mer) primers, and 2.5 units of *Taq* DNA polymerase. The PCR reaction mixture was denatured at 94°C for 5 minutes followed by 30 cycles of 94°C/45 seconds, 10 50°C/1 minute, 72°C/90 seconds and is ended with a 5 minute extension at 72°C. 2 μ l of the PCR amplification products were used for a second run PCR re-amplification using primers H1S and R2A. A 0.6 kb PCR fragment was cloned using the TA Cloning Kit from Invitrogen and used as a probe to screen an aspen genomic library to obtain the Pt4CL2 genomic clone. Two primers 15 (2A, 5'-TCTGTCTAGATGATGTCGTGGCCACGG-3'; SEQ ID NO:13 and 2B, 5'-TTAGATCTCTAGGACATGGTGGTGGC-3'; SEQ ID NO:14) were designed based on the genomic sequence of Pt4CL2 around the deduced transcription start site and the stop codon. These primers were used to clone Pt4CL2 cDNA by RT-PCR, as described above using total RNA isolated from 20 shoot tips.

The DNA sequences of Pt4CL1 and Pt4CL2 cDNA were determined using Δ *Taq* Cycle Sequencing kit from Amersham.

- The Pt4CL1 cDNA has an open reading frame of 1605 bp which encodes a polypeptide of 535 amino acid residues with a predicted molecular weight of 25 58.498 kd and pI of 5.9. The nucleotide sequence of the aspen 4CL cDNA clone Pt4CL1 is set forth as SEQ ID NO:1. The deduced amino acid sequence for the aspen 4CL1 protein is set forth as SEQ ID NO:2.

- The Pt4CL2 cDNA has an open reading frame of 1710 bp which encodes a polypeptide of 570 amino acid residues with a predicted molecular weight of 30 61.8 kd and pI of 5.1. The nucleotide sequence of the aspen 4CL cDNA clone Pt4CL2 is set forth as SEQ ID NO:3. The deduced amino acid sequence for the aspen 4CL2 protein is set forth as SEQ ID NO:4.

The aspen Pt4CL1 cDNA shares a 55-69% identity at the nucleotide level and 57-76% identity at the amino acid level with previously reported 4CL cDNAs and genes, whereas the Pt4CL2 cDNA shares a 60-71% identity at the nucleotide level and 58-73% at the amino acid level with other 4CL cDNAs and
5 genes as set forth in the following table.

Table 1: Comparison of PtdCL1 and PtdCL2 nucleotide and predicted amino acid sequences to each other and other full length 4CL sequences.

| Gene | Comparison with PtdCL1 (%) | | | Comparison with PtdCL2 (%) | | |
|---------|----------------------------|------------------|--------------------|----------------------------|------------------|--------------------|
| | DNA Identity | Protein Identity | Protein Similarity | DNA Identity | Protein Identity | Protein Similarity |
| PtdCL1 | | | | 61.3 | 63.4 | 72.7 |
| PtdCL2 | 61.3 | 63.4 | 72.7 | | | |
| Le4CL1 | 64.5 | 71.2 | 78.1 | 61.8 | 64.6 | 73.4 |
| Le4CL2 | 64.1 | 57.3 | 67.7 | 71.1 | 73 | 77.5 |
| Nt4CL1 | 66 | 71.4 | 78.1 | 61.5 | 65.3 | 74.4 |
| Nt4CL2 | 64.1 | 75 | 78.1 | 62.1 | 66.8 | 76 |
| Os4CL1 | 59.2* | 59.8 | 70.2 | 59.6* | 57.7 | 69.5 |
| Os4CL2 | 54.9 | 57.7 | 67.3 | 63.9 | 66.5 | 73.8 |
| Pet4CL1 | 65.1 | 71.2 | 78.1 | 62 | 64.3 | 73.5 |
| Pet4CL2 | 65 | 71.4 | 78.1 | 62.9 | 64.5 | 73.5 |
| Ptd4CL1 | 66.6 | 73.7 | 78.2 | 64.5 | 66.6 | 75.8 |
| Ptd4CL2 | 67 | 74.2 | 81 | 63.4 | 64.7 | 73.3 |
| A4CL | 63.7 | 69.9 | 72.7 | 62.4 | 61.1 | 70.2 |
| Lp4CL | 60.1 | 64 | 73.9 | 62.3 | 67.9 | 77.8 |
| St4CL1 | 59.2* | 74 | 81.4 | 62.2* | 65.3 | 74.5 |
| Vp4CL | 65.2 | 75.5 | 81.6 | 61.5 | 66.5 | 74.1 |

PtdCL1 and Ptd4CL2: aspen 4CL

Le4CL1 and Le4CL2: lathyrus eranthos 4CL

Nt4CL1 and Nt4CL2: tobacco 4CL

Os4CL1 and Os4CL2: rice 4CL (* DNA sequence compared to Os4CL1 coding region only)

PC4CL1 and PC4CL2: Parsley 4CL

Ptd4CL1 and Ptd4CL2: hybrid poplar 4CL

A4CL: Arabidopsis 4CL

Lp4CL: lobolly pine 4CL

St4CL: potato 4CL (* DNA sequence compared to coding region only)

Vp4CL: vanilla 4CL

In a study to characterize lignification in aspen stems, it was observed that the lignin composition in the top four internodes (referred to as top internodes hereafter) was different from that in the fifth and subsequent internodes, suggesting the involvement of developmentally regulated differential expression of lignin pathway genes during the transition from primary to secondary growth in aspen stem. To investigate whether this transition regulates differential expression of 4CL gene members, 4CL genes were cloned from top and lower (6th-10th) internodes and secondary-developing xylem tissue of aspen stems. Nucleotide sequence analysis revealed that clones derived from lower internodes were identical to Pt4CL1, whereas clones isolated from top internodes could be divided into two groups (T1 and T2). Clones in Group T1 were found identical to Pt4CL1. Clones in group T2 shared 60-75% sequence homology with other plant 4CL genes but were distinct from Pt4CL1 cDNA and designated as Pt4CL2-600. These results together with Northern hybridization analysis suggested that Pt4CL2-600 represents a fragment of another aspen 4CL gene expressed in top internodes.

The results of sequence analysis, phylogenetic tree and genomic Southern blot analysis indicate that Pt4CL1 and Pt4CL2 cDNAs encode two distinct 4CLs that belong to two divergent gene families in aspen. The deduced amino acid sequence for the Pt4CL2 protein contains a longer N-terminal sequence than the Pt4CL1 protein but shows profound similarity in the central and C-terminal portions of protein to the Pt4CL1 protein.

Pt4CL1 and Pt4CL2 cDNAs display distinct tissue-specific expression patterns. The Pt4CL1 sequence is expressed highly in the secondary developing xylem and in the 6th to 10th internodes whereas the Pt4CL2 sequence is expressed in the shoot tip and leaves. These tissue-specific expression patterns were further investigated by fusing promoters of Pt4CL1 and Pt4CL2 genes to a GUS reporter gene. The tissue specific promoters for Pt4CL1 and Pt4CL2 are discussed in more length below.

The substrate specificity of Pt4CL1 and Pt4CL2 is also different from each other as determined using recombinant proteins produced in *E. coli*.

Pt4CL1 utilized 4-coumaric acid, caffeic acid, ferulic acid and 5-hydroxyferulic acid as substrates. Pt4CL2 showed activity for 4-coumaric acid, caffeic acid and ferulic acid but not to 5-hydroxyferulic acid.

Specifically, Pt4CL1 and Pt4CL2 were used to construct expression
5 vectors for *E. coli* expression. The substrate specificity of Pt4CL1 and Pt4CL2 was tested using fusion proteins produced in *E. coli*. Two plasmids, pQE/4CL1 and pQE/4CL2, were constructed in which the coding regions of Pt4CL1 and Pt4CL2, respectively, were fused to N-terminal His tags in expression plasmids pQE-31 and pQE-32 (QIAGEN, Chatsworth, CA). The recombinant proteins of
10 Pt4CL1 and Pt4CL2 produced by *E. coli* were approximately 60 kD and 63 kD, respectively.

The two recombinant proteins were tested for their activity in utilizing cinnamic acid derivatives. Pt4CL1 recombinant protein showed 100, 51, 72, 19 and 0% relative activity to 4-coumaric acid, caffeic acid, ferulic acid, 5-
15 hydroxyferulic acid and sinapic acid, respectively. Pt4CL2 recombinant protein exhibited 100, 31, 26, 0 and 0% relative activity to 4-coumaric acid, caffeic acid, ferulic acid, 5-hydroxyferulic acid and sinapic acid, respectively. Neither recombinant protein showed detectable activity to sinapic acid.

The results of the tissue-specific expression pattern and substrate
20 specificity suggests that in addition to the general function of 4CL, Pt4CL1 apparently is more related to lignin synthesis in the xylem tissue and Pt4CL2 apparently is more likely involved in flavonoid synthesis and UV protection.

It should be noted that the isolation and characterization of the Pt4CL1 and Pt4CL2 cDNA clones is described in Kawaoka et al., Proceedings of the 6th
25 International Conference on Biotechnology in the Pulp and Paper Industry, Vienna, Austria (1995); and in Hu, Wen-Jing, Isolation and Characterization of 4-coumarate: Coenzyme A Ligase cDNAs and Genes from Quaking Aspen (*Populus tremuloides* Michx), Ph.D. Dissertation, Michigan Technological University, Houghton, Michigan (1997); and Tsai et al., Plant Physiol., 117, 101
30 (1998).

C. Transformation and Regeneration

Several methods for gene transformation of plant species with the 4CL sequence are available such as the use of *Agrobacterium*, electroporation, particle bombardment with a gene gun or microinjection.

5 Preferably, a 4CL cDNA clone is positioned in a binary expression vector in an antisense orientation under the control of double cauliflower mosaic virus 35S promoter. The vector is then preferably mobilized into a strain of *Agrobacterium* species such as *tumefaciens* strain C58/pMP90 and is used as the DNA delivery system due to its efficiency and low cost.

10 For example, with reference to Fig. 2, the binary expression pA4CL1 used for plant transformations is shown. Specifically, the Pt4CL1 cDNA is inserted in an antisense orientation into *Pac* I and *Bam*H I sites between the double CaMV 35S/AMV RNA4 and the 3' terminator sequence of the nopaline synthase gene in a binary cloning vector pA4CL1 (Fig. 2). The binary vector
15 containing hygromycin phosphotransferase (*HPT*) gene is modified from pBin 19. The gene construct pA4CL1 is available from Michigan Technological University, Institute of Wood Research, Houghton, Michigan.

The binary vector construct is mobilized into *Agrobacterium tumefaciens* using the freeze-thaw method of Holsters et al., Mol. Gen. Genet. 163: 181-187
20 (1978). For the freeze-thaw method, 1.5 ml of overnight cultures *Agrobacterium tumefaciens* strain C58/pMP90 is pelleted at 5000 x g for 3 minutes at 4°C and suspended in 1 ml of ice cold 20 mM CaCl₂. To the suspension is added 10 µl binary vector DNA (from an alkaline lysis minipreparation) and mixed by pipetting. The microcentrifuge tube is then frozen in liquid nitrogen for 5
25 minutes and thawed at 37°C for 5 minutes. After being cooled on ice, 1 ml of LB is added and the mixture is incubated at 28°C for 2 hours with gentle shaking. 200 µl of the cells is spread onto LB plates containing gentamycin and kanamycin and incubated at 28°C for 2 days. Colonies grown on the selection plates are randomly picked or miniprep and restriction enzyme digestion analysis
30 is used to verify the integration.

The resulting binary vector containing *Agrobacterium* strain is used to transform quaking aspen according to Tsai et al., Plant Cell Rep. 14: 94-97 as set forth below.

- 5 Explants of young leaves from cuttings of aspen are obtained by cutting leaf disks of approximately 7 mm square from the young leaves along the midrib of the leaves. The explants are surface sterilized in 20% commercial bleach for 10 minutes followed by rinsing 3 times with sterile distilled, deionized water.

- All of the culture media used includes the basal medium of woody plant medium (WPM) as described in Lloyd et al., Proc. Int. Plant Prop. Soc. 30: 421-
10 437 (1980) and supplemented with 2% sucrose. 650 mg/L calcium gluconate and 500 mg/L MES are added as pH buffers as described in Tsai et al., Plant Cell Reports, 1994. All culture media is adjusted to pH 5.5 prior to the addition of 0.75% Difco Bacto Agar and then autoclaved at 121 °C and 15 psi for 20 minutes. Filter sterilized antibiotics are added to all culture media after
15 autoclaving. All culture media are maintained at $23 \pm 1^\circ\text{C}$ in a growth chamber with 16 hour photoperiods ($160 \mu\text{E} \times \text{m}^{-2} \times \text{S}^{-1}$) except for callus induction (as will be described later) which is maintained in the dark.

- The sterilized explants are then inoculated with the mobilized vector with an overnight-grown agrobacterial suspension containing 20 μM acetosyringone.
20 After cocultivation for 2 days, the explants are washed in 1 mg/ml claforan and ticarcillin for 2 hours with shaking to kill *Agrobacterium*. The explants are blotted dry with sterile Whatman No. 1 filter paper and transferred onto callus induction medium containing 50 mg/L kanamycin and 300 mg/L claforan to induce and select transformed callus. The callus induction medium is the basal
25 medium with the addition of 6-benzyladenine (BA) and 2, 4-dichlorophenoxyacetic acid (2, 4-D) at concentrations of 0.5 mg/L and 1 mg/L, respectively, to induce callus.

- The kanamycin-resistant explants are then subcultured on fresh callus induction media every two weeks. Callus formation occurs after approximately
30 four weeks. Formed calli are separated from the explant and subcultured periodically for further proliferation.

When the callus clumps reach approximately 3 mm in diameter, the callus clumps are transferred to shoot regeneration medium. The shoot regeneration medium is the basal medium containing 50 mg/L kanamycin, 0.5 mg/L thidiazuron (TDZ) as a plant growth regulator and claforan at 300 mg/L to
5 kill *Agrobacterium*. Shoots were regenerated about 4 weeks after callus is transferred to regeneration medium.

As soon as the shoots are regenerated, they are immediately transferred to hormone-free elongation medium containing 50 mg/L kanamycin and, whenever necessary, claforan (300 mg/L), to promote elongation. Green and healthy
10 shoots elongated to 2-3 cm in length are excised and planted separately in a hormone-free rooting medium containing 50 mg/L kanamycin. The efficient uptake of kanamycin by shoots during their rooting stage provides the most effective selection for positive transformants. Transgenic plants are then transplanted into soil medium of vermiculite:peatmoss:perlite at 1:1:1 and grown
15 in the greenhouse.

The above described transformation and regeneration protocol is readily adaptable to other plant species. Other published transformation and regeneration protocols for plant species include Danekar et al., *Bio/Technology* 5:587-590 (1987); McGranahan et al., *Bio/Technology* 6:800-804 (1988);
20 McGranahan et al., *Plant Cell Reports* 8:512-616 (1990); Chen, Ph.D. Thesis, North Carolina State University, Raleigh, North Carolina (1991); Sullivan et al., *Plant Cell Reports* 12:303-306 (1993); Huang et al., *In Vitro Cell Dev. Bio.* 4:201-207 (1991); Wilde et al., *Plant Physiol.* 98:114-120 (1992); Minocha et al., 1986 Proc. TAPPI Research and Development Conference, TAPPI Press,
25 Atlanta, pp. 89-91 (1986); Parsons et al., *Bio/Technology* 4:533-536 (1986); Fillatti et al., *Mol. Gen. Genet* 206:192-199 (1987); Pythoud et al., *Bio/Technology* 5:1323-1327 (1987); De Block, *Plant Physiol.* 93:1110-1116 (1990); Brasileiro et al., *Plant Mol. Bio* 17:441-452 (1991); Brasileiro et al., *Transgenic Res.* 1:133-141 (1992); Howe et al., *Woody Plant Biotech.*, Plenum
30 Press, New York, pp. 283-294 (1991); Klopfenstein et al., *Can. J. For. Res.* 21:1321-1328 (1991); Leple et al., *Plant Cell Reports* 11:137-141 (1992); and Nilsson et al., *Transgenic Res.* 1:209-220 (1992).

D. Phenotype Changes

The results of the transformation can be confirmed with conventional PCR and Southern analysis. Transferring 4CL cDNA in an antisense orientation down regulates 4CL in the plant. Expression of the 4CL has been found to be blocked up to 96 percent of 4CL enzyme activity in some transgenic plants.

In the aspen example, after acclimation, the transgenic aspen displayed an unusual phenotype, including big curly leaves, thick stem diameter, longer internodes, more young leaves in the shoot tip and a red pigmentation in the petioles extending into midvein leaves. Red coloration of the developing secondary xylem tissues is observed after peeling of the bark in the transgenic plants.

E. Accelerated Growth

Down regulation of 4CL altered growth of the transgenic plants. For example, transformation with an antisense 4CL sequence accelerated the growth of the plant. Enhanced growth is markedly noticeable at all ages. In particular the transgenic trees showed enhanced growth in the form of thicker stems and enlarged leaves as compared to control plants. These characteristics are retained in the vegetative propagules of these transgenic trees. Table 2 sets forth exemplary data with respect to several lines of transgenic quaking aspen grown in the greenhouse after eight months. Volume represents the overall quantitative growth of the plant.

Table 2: Growth Measurement for Control and Transgenic Plants

| Plant # | Height (cm) | Diameter (cm)* | Volume (cm ³)* | Average Length of Internode (cm) |
|-----------|----------------|-------------------|-------------------------------|-------------------------------------|
| Control 1 | 247.7 | 1.08 | 75.6 | 2.6 |
| Control 2 | 250.2 | 1.01 | 66.8 | 2.8 |
| 11-1 | 304.8 | 1.15 | 105.5 | 3.1 |
| 11-2 | 248.9 | 1.08 | 66.4 | 3.4 |
| 11-3 | 241.3 | 0.84 | 44.6 | 3.2 |
| 11-4 | 288.3 | 0.84 | 66.7 | 3.4 |
| 11-5 | 246.4 | 0.92 | 54.6 | 3.3 |
| 11-7 | 226.7 | 1.13 | 75.7 | 3.3 |
| 11-8 | 289.6 | 1.16 | 102.0 | 3.3 |
| 11-4 | 287.0 | 1.76 | 232.6 | 4.3 |
| 11-10 | 252.7 | 0.84 | 45.6 | 3.1 |
| 11-11 | 247.7 | 0.86 | 48.0 | 3.5 |
| 12-1 | 247.7 | 1.1 | 78.4 | 2.7 |
| 12-2 | 199.4 | 0.96 | 48.1 | 2.5 |
| 12-6 | 294.6 | 0.92 | 65.2 | 3.2 |
| 16-1 | 227.3 | 0.95 | 53.7 | 2.8 |
| 16-2 | 278.1 | 0.97 | 68.5 | 3.4 |
| 16-3 | 265.4 | 1.09 | 82.5 | 3.5 |
| 17-2 | 243.8 | 0.89 | 50.5 | 2.6 |

* at 10 cm above ground

The averages for height, diameter, volume and average length between internodes for the control plants are as follows:

Height (cm) 248.95

Diameter (cm) 1.045

Volume (cm³) 71.2

Ave. Length of Internodes (cm) 2.7

With respect to height alone, for those transgenic plants (11-1, 11-4, 11-8, 11-9, 12-6, 16-2, 16-3) having a statistically larger height than the control plants, the average height was 286.83 cm as compared to the control plant average height of 248.95 cm.

With respect to diameter alone, for those transgenic plants (11-1, 11-7, 11-8, 11-9) having a statistically larger diameter than the control plants, the average diameter was 1.30 cm as compared to the control plant average diameter of 1.045 cm.

- 5 With respect to volume alone, for those transgenic plants (11-1, 11-8, 11-9, 12-1, 16-3) having a statistically larger volume than the control plants, the average volume was 120.2 cm³ as compared to the control plant average volume of 71.2 cm³.

- 10 With respect to average length of internodes alone, for those transgenic plants (11-1, 11-2, 11-3, 11-4, 11-5, 11-7, 11-8, 11-9, 11-10, 12-6, 16-2, 16-3) having a statistically larger average length of internodes than the control plants, the average length of internodes was 3.39 cm as compared to the control plant average length of internodes of 2.7° cm.

- 15 As demonstrated in Table 2, while there are variations in growth among the transgenic plants, the average length of the internodes for the transgenic plants is consistently and significantly higher than that of the control plants. Moreover, there is also faster root initiation, and alterations, e.g., an increase, in root fresh weight and length, i.e., enhanced root growth. Variations in the growth of the transgenic plants is normal and to be expected. Preferably, a
20 transgenic plant with a particular growth rate is selected and this plant is vegetatively propagated to produce an unlimited number of clones that all exhibit the identical growth rate.

F. Lignin

- 25 Down regulation of lignin pathway 4CL results in production of plants with reduced lignin content.

The following table shows the reduction of lignin content and 4CL enzyme activity in several transgenic aspen which were transformed with a homologous antisense 4CL sequence.

Table 3: Characterization of Transgenic Aspen Plants Harboring Antisense 4CL Sequence

| Transgenic Plant # | Lignin Content % Based on Wood Weight | % Lignin Reduction | %4CL Enzyme Activity* | % 4CL Enzyme Activity Reduction |
|--------------------|---------------------------------------|--------------------|-----------------------|---------------------------------|
| Control | 21.4 | 0.0 | 868 | 9 |
| 11-1 | 20.5 | 4.2 | 1171 | -25 |
| 11-2 | 19.2 | 10.3 | 515 | 45 |
| 11-3 | 20.9 | 2.3 | 922 | 9 |
| 11-4 | 19.7 | 7.9 | 1032 | -19 |
| 11-5 | 19.7 | 7.9 | 691 | 20 |
| 11-7 | 19.4 | 7.9 | 578 | 38 |
| 11-8 | 20.2 | 5.6 | 694 | 20 |
| 11-9 | 20.4 | 4.7 | 806 | 14 |
| 11-10 | 19.4 | 9.3 | 455 | 51 |
| 11-11 | 20.4 | 4.7 | 726 | 22 |
| 12-1 | 12.8 | 40.2 | 49 | 95 |
| 12-2 | 12.6 | 41.1 | 62 | 93 |
| 12-3 | 11.9 | 44.4 | 61 | 94 |
| 12-6 | 19.4 | 7.5 | 786 | 16 |
| 16-1 | 12.8 | 40.2 | 35 | 96 |
| 16-2 | 20.6 | 3.7 | 786 | 17 |
| 16-3 | 20.6 | 1.9 | 795 | 15 |
| 17-1 | 20.5 | 4.2 | 855 | 9 |
| 17-2 | 21.4 | 0.0 | 925 | 1 |

*activity is expressed as pkat/(mg protein) using 4-coumaric acid as the substrate

Lignin content was determined according to Chiang and Funaoka (1990) Holzforschung 44:147-155. 4CL enzyme activity was determined according to Ranjeva et al. (1976), Biochimie 58:1255-1262.

The data in Table 3 demonstrates a correlation between down regulation of 4CL and reduction in lignin content. Transgenic plants with reduced lignin content have an altered phenotype in that the stem is more elastic to the touch or less curly.

It should also be noted that for those transgenic plants (12-1, 12-2, 12-3 and 16-1) with the approximately 40% reduction in lignin content and the corresponding approximately 95% reduction in 4CL enzyme levels, all of those transgenic plants had a consistent deep red coloration in the wood of the plant.

- 5 Accordingly, the deep red color can be used as an identifier of reduced lignin content.

- Down regulation of lignin pathway 4CL can also result in production of plants with an altered lignin structure. Based upon thioacidolysis (Rolando et al. (1992) Thioacidolysis, Methods in Lignin Chemistry, Springer-Verlag, Berlin, 10 pp. 334-349) of plants 12-3 and 16-1, coniferyl alcohol and sinapyl alcohol lignin units are significantly reduced in these two plants as compared to the control tree, as shown in the following table.

Table 4: Altered Lignin Structure

| | | | |
|----|---------|---------------------------|------------------------|
| 15 | Plant # | Coniferyl Alcohol Units * | Sinapyl Alcohol Units* |
| | Control | 733 | 1700 |
| | 12-3 | 283 | 592 |
| | 16-1 | 247 | 445 |

*micro-mole/g of lignin

- 20 The alteration of the frequency of the structural units in lignin of these transgenic plants is evidence that the overall structure of lignin in these plants has been genetically altered.

G. Cellulose Content

- Down regulation of lignin pathway 4CL can result in increased cellulose 25 content of the transgenic plants. Analysis of control and transgenic aspen for carbohydrate content demonstrate a higher cellulose content in the transgenic plants than the control plants. Particularly, the transgenic plants that have over 40% lignin reduction have about 10-15% higher cellulose content than the control. Data is set forth in the following tables for trees that were transformed 30 with homologous 4CL in an antisense orientation:

Table 5: Analysis of Carbohydrate Components in Transgenic and Control Aspen

| Plant # | Glucan | Arabinan | Galactan | Rhamnan | Xylan | Mannan |
|---------|--------|----------|----------|---------|--------|--------|
| Control | 44.23% | 0.47% | 0.79% | 0.37% | 17.19% | 1.91% |
| 11-2 | 49.05% | 0.36% | 1.05% | 0.38% | 15.34% | 2.04% |
| 11-9 | 45.95% | 0.40% | 0.80% | 0.37% | 17.12% | 1.83% |
| 11-10 | 47.49% | 0.43% | 0.99% | 0.40% | 16.24% | 2.35% |
| 12-3 | 50.83% | 0.55% | 1.24% | 0.40% | 17.25% | 1.77% |
| 16-1 | 48.14% | 0.56% | 1.07% | 0.48% | 19.14% | 1.58% |
| 16-2 | 46.55% | 0.34% | 0.82% | 0.37% | 16.75% | 2.31% |

Table 6: Comparison of Lignin and Cellulose (glucan) Contents in Transgenic and Control Aspen

| Plant # | Lignin | | Cellulose | |
|---------|-------------------|-------------|-------------------|------------|
| | Content % on Wood | % Reduction | Content % on Wood | % Increase |
| Control | 21.4 | 0 | 44.23 | 0 |
| 11-2 | 19.2 | 10.3 | 49.05 | 10.9 |
| 11-9 | 20.4 | 4.7 | 45.95 | 3.9 |
| 11-10 | 19.3 | 9.3 | 47.49 | 7.4 |
| 12-3 | 11.9 | 44.5 | 50.83 | 14.9 |
| 16-1 | 12.8 | 40.2 | 48.14 | 8.8 |
| 16-2 | 20.6 | 3.7 | 46.55 | 5.2 |
| 11-6 | 18.6 | 13.1 | 45.98 | 3.8 |
| 12-1 | 12.5 | 40.2 | 48.35 | 9.3 |
| 12-2 | 12.6 | 41.1 | 49.74 | 12.5 |
| 12-5 | 14.4 | 32.7 | 45.58 | 3.1 |

The procedure for carbohydrate analysis utilized is as follows. About 100 mg of milled woody tissue powder with sizes that pass a 80-mesh screen was hydrolyzed with 1 mL of 72% (W/W) H₂SO₄ for 1 hr at 30°C. Samples were then diluted to 4% (W/W) H₂SO₄ with distilled water, fucose was added as

an internal standard, and a secondary hydrolysis was performed for 1 hr at 121 °C. After secondary hydrolysis, the sugar contents of the hydrolysates are determined by anion exchange high performance liquid chromatography using pulsed amperometric detection. Sugar contents are expressed as % of the weight of the woody tissue used. The above procedures are similar to those in a publication by Pettersen and Schwandt, J. Wood Chem & Technol. 11:495-501 (1991).

H. Increased Disease Resistance

Down regulation of lignin pathway 4CL can result in altered levels of phenylpropanoids or secondary metabolites that display antimicrobial activity. Thus, transgenic plants with down-regulated 4CL can result in enhanced disease resistance, and in particular, with increased fungal pathogen resistance. In particular, greenhouse transgenic aspen plants may show a disease resistance to fungi such as those which induce leaf-blight disease.

I. Promoters

Two distinct genes encoding 4CL and their promoters were cloned. The promoter of Pt4CL1 can drive gene expression specifically in xylem tissue and the promoter for Pt4CL2 confers gene expression exclusively in the epidermal tissues. These promoters can be used to manipulate gene expression to engineer traits of interest in specific tissues of target plants. The significance of the promoters is the application of the xylem-specific promoter to direct the expression of any relevant genes specifically in the xylem for engineering lignin content, lignin structure, enhanced growth, cellulose content, other value-added wood qualities, and the like. The importance of the epidermis-specific promoter is its ability to drive the expression of any relevant genes specifically in epidermal tissues for engineering disease-, UV light-, cold-, heat-, drought-, and other stress resistance traits in plants.

Specifically, the promoters of the Pt4CL1 and Pt4CL2 were isolated as follows. An aspen genomic library was screened with Pt4CL1 cDNA and Pt4CL2 partial cDNA fragment to isolate genomic clones of Pt4CL1 and Pt4CL2. Eleven and seven positive genomic clones were identified for Pt4CL1 and Pt4CL2 gene, respectively. Among 11 positive clones for Pt4CL1,

Pt4CL1g-4 contained a full length coding sequence and at least 2 kb of 5' flanking regions. The restriction map of Pt4CL1g-4 is set forth at Fig. 3.

With respect to Pt4CL2, restriction map analysis was performed on λ DNA of positive genomic clone Pt4CL2g-11 which contains a full length
5 coding sequence and about 1.2 kb of 5' flanking region. The restriction map of Pt4CL2g-11 is set forth at Fig. 4.

Approximately a 2.3 kb 5' flanking region of Pt4CL1 was digested from Pt4CL1g-4 using *Xba* I and *Sac* I sites and cloned into pGEM7Z *Xba* I and *Sac* I sites. The subcloned Pt4CL1 promoter was named p7Z-4XS and the restriction
10 map of P7Z-4XS is set forth at Fig 5. The 5' unilateral deletion of p7Z-4XS was generated for DNA sequencing by exonuclease III/S1 nuclease digestion using Erase-a-Base System (Promega, Madison, WI). The deletion series was sequenced using a primer on pGEM7Z vector.

A 1.5 kb *Hind* III and *Eco*R I fragment containing a 1.2 kb 5' flanking
15 region of Pt4CL2 and 0.3 kb coding region of Pt4CL2g-11 was subcloned in pBluescript II SK+ *Hind* III and *Eco*R I sites. The restriction map of the resulting clone, pSK-11HE, was determined by digesting the plasmid with several restriction enzymes, as in set forth at Fig. 6. In order to determine the sequence of the Pt4CL2 promoter, pSK-11HE was further digested into small
20 fragments according to the restriction map and subcloned into vectors with suitable cloning sites. The DNA sequence was determined using M13 universal primer and reverse primer on the vector.

The DNA sequences of the two promoters was determined and analyzed using Δ Taq cycle sequencing Kit (USB, Cleveland, OH), and GENETYX-MAC
25 7.3 sequence analysis software from Software Development Co., Ltd. The nucleotide sequence of promoter region of Pt4CL1 is set forth as SEQ ID NO:5 and the nucleotide sequence of the promoter region of Pt4CL2 is set forth as SEQ ID NO:6. The sequence of the promoter regions of Pt4CL1p and Pt4CL2p is available from Genbank, Accession Nos. AF041051 and AF041052,
30 respectively.

The insignificant sequence similarity between the 5'- and 3'-noncoding regions of these two genes and their distinct exon-intron organizations (four

introns in Pt4CL1 and five in Pt4CL2) further substantiate their functional and perhaps evolutionary divergency. Striking differences also were observed in the promoter sequences of these two genes. Three cis-acting elements, box P (CCTTTCACCAACCCCC; SEQ ID NO:15), box A (CCGTTC; SEQ ID NO:16), and box L (TCTCACCAACC; SEQ ID NO:17), previously shown to be consensus in all known plant phenylalanine ammonialyase (PAL) and 4CL gene promoters (Hahlbrook et al., Proc. Natl. Acad. Sci. USA, 92, 4150 (1995); Logemann et al., Proc. Natl. Acad. Sci. USA, 92, 5905 (1995)), were identified within the 1kb 5' flanking sequence of Pt4CL1 (GenBank Accession No. AF041051). However, none of these boxes could be found within the analyzed 1.2 kb 5' flanking region of Pt4CL2 (GenBank Accession No. AF041052), suggesting that promoter differences between Pt4CL1 and Pt4CL2 genes could be responsible for the strikingly different patterns of tissue-specific expression of these genes, as observed in Northern analysis.

Tissue-specific expression can be achieved by fusing the promoters of Pt4CL1 or Pt4CL2 to a gene, e.g., an open reading frame of interest and transferred to a plant species via *Agrobacterium*. For the sake of example, the promoters of Pt4CL1 and Pt4CL2 were fused to a GUS reporter gene as detailed below. However, it should be noted that genes other than the GUS reporter gene can be fused to these promoters for tissue specific expression.

In order to construct Pt4CL1 promoter-GUS binary vector, a 1 kb fragment covering 5'-flanking region and 17 bp coding region of Pt4CL1 was subcloned into pGEM7Z *Sph* I and *Eco*R I sites for constructing promoter-GUS binary vector. In this 1 kb DNA fragment, it is found that one *Xho* I site is located at 486 bases upstream to the translation start site and the *Eco*R I site is located at 17 bases downstream the translation start site. This 0.6 kb fragment was subcloned into pGEM7Z *Xho* I and *Eco*R I sites and used as a template in PCR amplification.

In order to construct a promoter-GUS transcriptional fusion, a *Bam*H I site was introduced in front of the translation start site of Pt4CL1 by PCR. PCR amplification was performed using p7Z-4XE as the template, M13 universal primer on pGEM7Z vector as 5' end primer and Pt4CL1p-1 primer containing a

*Bam*H I site at the end is complementary to a sequence upstream of the translation start site. The reaction was carried out in 100 µl reaction mix containing 1x *pfu* reaction buffer, 200 µl each dNTPs, 100 µM each primer and 5 units of *pfu*. The PCR reaction mixture was denatured at 94°C for 5 minutes
5 followed by 30 cycles of 94°C (1 minute), 55°C (1 minute), 72°C (1 minute, 30 seconds) and was ended with a 5 minute extension at 72°C.

The amplified 0.6 kb fragment was cloned and sequenced to confirm the sequence. The engineered 0.6 kb fragment was ligated to p7Z-4SE which was digested with *Xho* I and *Bam*H I. In order to incorporate a *Hind* III site in the 5'
10 end of Pt4CL1 promoter, the 1 kb *Sph* I-*Bam*H I Pt4CL1 promoter region was the cloned into pNoTA (5 prime – 3 prime Inc., Boulder, CO) *Sph* I and *Bam*H I site. The 1 kb Pt4CL1 promoter was then released from pNoTA vector with *Hind* III and *Bam*H I digestion and subsequently transcriptionally fused to pBI101 *Hind* III and *Bam*H I sites in front of GUS. The resulting binary vector was
15 named Pt4CL1p-GUS and is set forth at Fig. 7.

In order to construct Pt4CL2 promoter-GUS binary vector, pSK-11HE was digested with *Sph* I and *Eco*R I to release 0.2 kb *Sph* I and *Eco*R I fragment. The 0.2 kb fragment was cloned into pGEM7Z *Sph* I and *Eco*R I sites. A primer, Pt4CL2p-3' (5'-CATCGGATCCTGAGATGGAAGGGAGTTTCT-3'; SEQ ID
20 NO:15) was designed to be complementary to a sequence upstream of the translation start site of Pt4CL2 and to incorporate *Bam*H I site at the end. Amplification was performed using p7Z11SE as a template, M13 universal primer as the 5' end primer and Pt4CL2p-3 as the 3' end primer. A PCR reaction was carried out and the amplified PCR product was cloned and
25 sequenced to check the fidelity of the PCR amplification. The 0.2 kb *Sph* I-*Bam*H I DNA fragment with correct sequence was fused to pSK-11HE linearized with *Sph* I and *Bam*H I. The resulting plasmid was named pSK-11HB. The promoter of Pt4CL2 was then excised from pSK-11HB with *Hind* III and *Bam*H I and ligated to pBI101 and *Hind* III and *Bam*H I site to make Pt4CL2p-GUS
30 transcriptional fusion binary vector as shown in Fig. 8.

The Pt4CL1p-GUS and Pt4CL2p-GUS constructs were then mobilized into *Agrobacterium tumefaciens* strain C58/pMP90 by freeze and thaw method as explained previously.

- Leaf disk transformation of tobacco with these two *Agrobacterium* constructs is conducted according to the method of Horsch R.B. (1988) Leaf Disk Transformation, Plant Molecular Biology Manual, A5:1-9.

- To further investigate the regulation of the tissue-specific expression of Pt4CL1 and Pt4CL2 genes at the cellular level, their promoter activities were analyzed in transgenic tobacco plants by histochemical staining of GUS gene expression driven by a 1 kb Pt4CL1 and 1.2 kb Pt4CL2 promoter sequences, respectively. In Pt4CL1p-GUS transgenic plants, intense GUS staining was detected in lignifying xylem of stem. Strong GUS activity also was found localized to xylem of leaf mid-rib and of root. However, there was no GUS expression in leaf blade, stem epidermis, cortex, phloem and pith, and flower petal. These results are consistent with the evidence that Pt4CL1 gene expression is xylem- or lignifying tissue-specific, and with the observation that Pt4CL1 mRNA level is the highest in aspen secondary developing xylem. In striking contrast to the Pt4CL1 promoter activity, the Pt4CL2 promoter did not direct GUS expression in vascular and xylem tissues in the stem and the leaf of Pt4CL23p-GUS transgenic plants. Instead, it directed GUS expression in lignin-deficient epidermal cells of the stem (Figure 10C) and of the leaf, reflecting the association of Pt4CL2 with nonlignin-related phenylpropanoid biosynthesis in the plant's outer layers. In addition, GUS staining also was detected in Pt4CL2p-GUS transgenic plant's floral organs, such as stigma and petal, suggesting the likely relevance of Pt4CL2 in mediating the formation of flavonoids, which are known to be accumulated in these organs (Higuchi (1997, supra; Caldwell et al., *Physiol. Plant*, 58, 455 (1983); Shirley, *Trends in Plant Sci.*, 1, 377 (1996)).

- The epidermis-specific Pt4CL2 promoter activity indicated that the in vivo Pt4CL2 mRNA message observed in aspen stem internodes could be caused by the signal derived from the epidermis RNA. Thus, the specific expression of

Pt4CL2 mRNA in epidermis further supports the biochemical functions of Pt4CL2 protein in the biosynthesis of nonlignin-related phenylpropanoids.

Therefore, the promoter fragments incorporated in Pt4CL1p-GUS and Pt4CL2p-GUS fusion genes must encompass the regulatory sequence elements that are responsible for the contrasting tissue-specific expression between Pt4CL1 and Pt4CL2 genes in aspen. Thus, based on both *in vivo* gene expression and gene promoter activity analyses, it was concluded that the expression of Pt4CL1 and Pt4CL2 genes in aspen is compartmentalized.

These results demonstrate that in aspen two functionally distinct 4CLs are uniquely compartmentalized by their gene regulatory systems for mediating differentially the biosynthesis of lignin and other phenylpropanoids that serve different physiological functions in aspen. Pt4CL1 is involved in channeling hydroxycinnamic acid derivatives to the synthesis of guaiacyl-syringyl lignin in xylem tissues. Pt4CL2 is associated with the biosynthesis of phenylpropanoids other than lignin in epidermal cells in the stem and the leaf, suggesting its likely participation in disease-resistance or defense-related mechanisms in the plant's outer layers. Therefore, 4CL isoforms may have distinct roles in plant defense systems and in lignification in a tissue-specific manner. From a practical point of view, the tissue-specific Pt4CL1 and Pt4CL2 gene promoters may offer a more defined control of future genetic engineering of traits in trees that must be confined to xylem or epidermal cells.

J. Cellulose Accumulation

Twenty-five transgenic aspen lines were generated in which Pt4CL1 expression was down-regulated to various degrees by antisense inhibition, using a Pt4CL1 gene operatively linked to a duplicated enhancer CaMV 35S promoter (Datla et al., Plant Sci., 94, 139 (1993)). The effect of Pt4CL1 deficiency on woody tissue development was investigated in ten-month-old trees. Pt4CL1 messenger RNA was drastically reduced in four lines (Fig. 9A). These lines also exhibited more than a 90% reduction in xylem Pt4CL1 enzyme activity (Fig. 9B), and a 40 to 45% reduction in stem lignin (Fig. 9C). A more modest lignin reduction was found in those lines with less drastic repression of Pt4CL1 activity. The reduction in lignin content was restricted to woody xylem, as

shown by attenuated lignin autofluorescence in xylem but not in phloem fibers following UV-irradiation (Figs. 9D, E). Severe repression of other lignin biosynthetic pathway enzymes, such as COMT or CAD, had no effect on lignin quantity in transgenic aspen, hybrid poplar or a loblolly pine (*Pinus taeda*)

- 5 mutant (Tsai et al., 1998; VanDoorselaere et al., *Plant J.*, 8, 855 (1995); Baucher et al., *Plant Physiol.*, 112, 1479 (1996)). Lignin structure, however, was significantly altered in these cases.

- To investigate the effect of Pt4CL1 repression on lignin structure, milled wood lignins were isolated from the stem of a transgenic (line 6 with a 45%
10 lignin reduction) and a control (using methods described in Bjorkman, *Nature*, 174, 1057 (1954); Chiang et al., *Holzforschung*, 44, 147 (1990); and Ralph et al., *JACS*, 116, 9448 (1994)) and then were analyzed by nuclear magnetic resonance (NMR) Examination of HSQC (heteronuclear single-quantum coherence) spectra (Fig. 10) and their HSQC-TOCSY (HSQC-total correlation
15 spectroscopy) counterparts and HMQC (heteronuclear multiple-quantum correlation) indicated that these lignins are structurally similar, consistent with their comparable syringyl-to-guaiacyl ratios based on thioacidolysis of intact stem. The ratios for control and transgenic line 6 were 2.3 and 2.1, respectively. Thus, there appeared to be little disruption of the normal lignin structure as a
20 result of reduced Pt4CL1 activity. It is clear from Figure 10 that β -aryl ethers (β -O-4) **10**, normally the most abundant (50 to 60%) linkage type in tree lignin (Adler et al., *Wood Sci. Technol.*, 11, 169 (1977)), predominate in both lignin samples. In both lignins, erythro-isomers are more prevalent than their threo-counterparts, typical of angiosperm lignin. Resinol (β - β) units (**12** Fig. 10),
25 which largely results from coupling of sinapyl alcohol **9b** monomers and represent initial intermediates in lignin polymerization reactions in angiosperm trees, are well represented in both lignins. Traces of phenylcoumaran (β -5) units **11** and α - β -diaryl ethers **14** were detectable in each lignin. Absent from both lignins were condensed biphenyl units such as dibenzodioxocins **13** (Ralph et al.,
30 *supra*). Such units, formed from 5-5-homo-coupling of coniferyl alcohol **9a**, normally represent about 4% of the constituents in angiosperm lignin (Adler, *supra*).

Low levels of 4-coumaric **2** and ferulic **4** acids are sometimes detectable in angiosperm lignins. Therefore, it was determined whether the incorporation of these acids was affected by decreased Pt4CL1 activity. Long-range ^{13}C - ^1H -correlation (HMQC) NMR experiments revealed that these acids were absent from both lignin samples. However, cell walls of transgenic stem tissue contained alkaline extractable 4-coumaric **2** and ferulic **4** acids at levels 11- and 5-fold higher, respectively, than the control. Alkaline hydrolysis of stem wood meal (pass 80-mesh) was performed at room temperature for 24 hr in 1 N NaOH (Hartley, J. Chromatogr., 54, 335 (1971)). The hydrolysates were neutralized, extracted with ethyl acetate and concentrated. The concentrated products were derivatized with BSTFA and analyzed by GC-MS in SIM (selected ion monitoring) mode using a DB-5 column. 4-Coumaric acid **2** (TMS-derivative; m/z 308) content of control was 199 ± 13 nmol/g dry wood, and 2145 ± 93 nmol/g dry wood in transgenic line 6. Ferulic acid **4** (TMS-derivative; m/z 338) contents in control and transgenic line 6 were 510 ± 9 and 2431 ± 120 nmol/g dry wood, respectively. No sinapic acid **6** (TMS-derivative; m/z 368) could be detected in control. However, a significant amount of sinapic acid, 2452 ± 119 nmol/g dry wood, was found in transgenic line 6.

Together, the lignin and cell wall analyses support a requirement for activation by Pt4CL1 of these phenolic acids for their incorporation into lignin. The cell wall apparently serves as a sink for accumulating these acids when Pt4CL1 activity is reduced. As a result, lignin content was reduced in the transgenic line but lignin composition and structure were not significantly altered. The conservation of normal lignin composition and structure in the transgenic aspen stands in sharp contrast to the marked changes of lignin composition and structure in other transgenic and mutant plants with altered lignin biosynthesis (Tsai et al., 1998; Van Doorsselaere et al., 1995; Baucher et al., 1996; Elkind et al., Proc. Natl. Acad. Sci. USA, 87, 9057 (1990); Piquemal et al., Plant J., 13, 17 (1998); Sewalt et al., Plant Physiol., 115, 41 (1997); Kajita et al., Plant Physiol., 114, 871 (1997); Lee et al., Plant Cell, 9, 1985 (1997); Dwivedi et al., Plant Mol. Biol., 26, 61 (1994); Ni et al., Transgenic Res., 3, 120 (1994); Atanassova et al., Plant J., 8, 465 (1995); Halpin et al., Plant J., 6, 339

(1994); Hibino et al., *Biosci. Biotech. Biochem.*, 59, 929 (1995)). The results are consistent with the supposition that 4CL modulates lignin accumulation in trees in a regulatory manner that does not result in disruption of lignin structure.

- Lignin and polysaccharides are proposed to account for the remarkable
- 5 mechanical strength of woody tissues (White et al., *Nature*, 205, 818 (1965); Atalla et al., *Science*, 227, 636 (1985); Houtman et al., *Plant Physiol.*, 107, 977 (1995); Taylor et al., *Plant J.*, 2, 959 (1992); Turner et al., *Plant Cell*, 9, 689 (1997)). In consideration of the possible effects of severe lignin reduction on structural polysaccharide components, these components were examined in stem
- 10 wood tissue. While hemicellulose content remained essentially unchanged, the transgenic lines had a 9 to 15% increase in glucan (Table 7), identified as β -(1-4)-glucan, or cellulose, by methylation-based linkage analysis and enzymatic hydrolysis. Lignin content was determined as the sum of Klason and acid-soluble lignins which represent the absolute quantity of lignin (Chiang et al.,
- 15 *Holzforschung*, 44, 147 (1990)). Cellulose and hemicelluloses contents were determined based on the total sugars after acid hydrolysis of these polysaccharides in stem woody tissue (Chiang et al., *Wood Sci. Technol.*, 17, 217 (1983); Pettersen et al., *J. Wood Chem. Technol.*, 11, 495 (1991)). Wood meal (pass 80-mesh) was vacuum-dried at 45°C and hydrolyzed with H₂SO₄.
- 20 Sugar contents of the hydrolysates were determined by anion exchange high performance liquid chromatography using pulsed amperometric detection and used for quantifying glucan and other polysaccharides (hemicelluloses) (Davis, J. *Wood Chem. Technol.*, 18, 235 (1998)).

- The dried wood meal was also used for methylation analysis of the
- 25 glucan in wood. Both the Hakomori (*J. Biochem. Tokyo*, 55, 205 (1964)) and NaOH/CH₃I (Ciucanu et al., *Carbohydr. Res.*, 131, 209 (1984)) methylation procedures were followed. Methylated samples were hydrolyzed in 2M TFA at 121°C for 2 hr, reduced with sodium borodeuteride, and acetylated using acetic anhydride at 120°C for 3 hr. The derivatized samples were analyzed by GC-MS
- 30 using a Sp2330 Supelco column. The methylation revealed that the glucose residues are mainly derived from 1-4 glucan for both control and transgenic

lines. Enzymatic hydrolysis of stem woody tissue further confirmed that the glucans in both control and transgenic lines are β -(1 \rightarrow 4)-glucan, or cellulose.

Thus, (1 \rightarrow 3)-linked glucan (callose), reportedly deposited in plant cell walls as a result of perturbed secondary metabolism (Schmelzer et al., Plant Cell, 1, 993 (1989)), was not detected in transgenic or control wood. Together, increased cellulose and decreased lignin content resulted in a cellulose-to-lignin ratio of 4 compared with 2 in control aspen (Table 7). The reason for the increased cellulose content is not clear. The absence of change in transcript levels of an aspen homolog of *celA* encoding a catalytic subunit of cellulose synthase (Arioli et al., Science, 279, 717 (1997)) argues against an increase in the rate of cellulose deposition due to altered transcriptional regulation in transgenic trees with reduced lignin content. The increase in cellulose content suggests that cross talk between lignin and cellulose biosynthetic pathways can nevertheless occur to ensure that cellulose biosynthesis becomes the preferred structural carbon sink when lignin biosynthesis is reduced. Because cellulose and lignin are the two components of wood most responsible for its rigidity, such cross talk could represent an adaptation to sustain mechanical strength in lignin deficient xylem.

The reduced lignin content in transgenic lines did not adversely affect tree growth and development. In fact, trees with down-regulated *Pt4CL1* had thicker stems, longer internodes, and larger (frequently epinastic) leaves than controls (Figs. 11A and 11B). Scanning electron microscopy (SEM) revealed that the shape and size of stem xylem fiber and vessel cells were similar to those of controls (Figs. 11C-F). Therefore, the enhanced stem development in these transgenic lines was apparently due to increased proliferative activity during xylem development rather than to increased cell size. Root growth rates also increased in these lines, resulting in greater length (15-fold) and fresh weight gain (20-fold) than in controls over a 14-day period in ex vitro rooting experiments (Fig. 11G). Cell size distribution in the meristematic and elongation zones of root tips was similar in control and transgenic roots. As was the case in stem xylem, increased root growth rate of the transgenic was due to increased cell number. Leaf growth also increased in the transgenic lines resulting in 4- to

5-fold larger leaves than in controls (Fig. 11B). Mature leaf adaxial epidermal cells were measured in two of the transgenic lines and found to be at least twice as large as in control aspen. A more detailed analysis was conducted to determine whether the rate and/or the duration of cell expansion accounted for the increased cell size in mature leaves of transgenic aspen. Epidermal cell expansion stopped at leaf number 15 below the first emerging leaf in control plants, but epidermal cells as well as leaf area continued to expand at leaf number 28 in transgenics (Fig. 11H). Therefore, the prolonged expansion of epidermal cells contributed to increased leaf size in the transgenic aspen lines.

The promotive effects on growth and development in the transgenic trees was a surprising observation. Growth enhancement has not been reported in transgenic tobacco or Arabidopsis with downregulated PAL (phenylalanine ammonia lyase), CCR, C4H, 4CL, COMT, or CAD. In fact, stunted growth and collapsed cell walls occurred in some transgenic tobacco with altered lignin biosynthesis. Whether the growth responses between herbaceous and tree species differed due to altered lignin biosynthesis per se is not clear. In the case of aspen, lignin composition and structure were conserved, eliminating the possibility that altered lignin constituents promoted growth. In aspen trees, reduced expression of Pt4CL1 disrupted lignin biosynthesis downstream of the phenylpropanoid pathway and this increased the concentration of phenylpropanoid intermediates in cell walls. At the same time, enhanced cell division and cell expansion were observed in root tips and leaves. Whether the growth enhancement observed in the transgenic aspen is due to altered carbon distribution between primary/secondary metabolism or specifically due to changes in wall-bound moieties are two possibilities to consider. Histone gene(s) expression has been used as a marker to show that cell division decreases in suspension cells and young leaves of parsley following treatments of that divert carbon flow in to the phenylpropanoid pathway and away from primary metabolic pathways (Logemann et al., Plant J., 8, 865 (1995)). There is also current interest in the organization and composition of cell wall constituents and their effects on cell expansion and plant growth. For these rationale,

phenylpropanoid flux as well as cell wall constituents would be of interest for investigating growth effects of lignin manipulation in trees.

- The finding that cellulose content increases in transgenic aspen with disrupted lignin biosynthesis is unique; similar observations have not been reported in herbaceous plants (Turner et al., *Plant Cell*, 9, 689 (1997); Elkind et al., 1990; Piquemal et al., 1998)). Interesting to consider is the idea that in perennial woody plants, lignin and cellulose deposition in cell walls are regulated in a compensatory fashion such that decreased in one are compensated for by increases in the other for maintaining the cellular structural integrity. This compensatory deposition of lignin and cellulose is consistent with the manner of how trees regulate their lignin and cellulose quantities in the course of forming naturally occurring reaction wood for mechanical support. Compensatory regulation such as this would also provide metabolic flexibility during annual growth increments, perhaps key for the long term structural integrity of woody perennials like trees. Further study is required to determine whether such regulation of cellulose accumulation is sensitive to primary/secondary metabolism and to changes in cell wall constituents such as those observed in Pt4CL1 down-regulated aspen.

- Overall, lignin limits the utilization of wood for fiber/material-, chemical-, and energy-production. Traditional breeding approaches have not led to trees with more desirable lignin/cellulose composition. However, genetic engineering appears to offer a strategy for manipulating such traits in trees, with the prospect of systemically regulating growth as reported here. The benefit of these engineered traits may also extend to forage crops in which lignin has been identified as the major barrier to their digestibility by ruminants.

Table 7. Lignin and cellulose contents in stem woody tissue of control and transgenic aspen. Data are the mean \pm SD of three independent experiments. Normalized values relative to control are shown in parentheses.

| | | | | |
|----|---------|------------------------|------------------------|---------------------------|
| | | Lignin Content | Cellulose Content | |
| 5 | Line | (% of dry wood weight) | (% of dry wood weight) | Cellulose-to-lignin ratio |
| | Control | 21.62 ± 0.30 (100) | 44.23 ± 0.43 (100) | 2.0 |
| | 4 | 12.83 ± 0.28 (60) | 48.35 ± 0.60 (109) | 3.8 |
| | 5 | 13.02 ± 0.28 (60) | 49.74 ± 0.45 (112) | 3.7 |
| | 6 | 11.84 ± 0.08 (55) | 50.83 ± 0.26 (115) | 4.3 |
| 10 | 8 | 12.90 ± 0.04 (60) | 48.14 ± 0.29 (109) | 3.8 |

All publications and patents are incorporated by reference herein, as though individually incorporated by reference, as long as they are not inconsistent with the present disclosure. The invention is not limited to the exact details shown and described, for it should be understood that many variations and modifications may be made while remaining within the scope of the invention defined by the claims.

WHAT IS CLAIMED IS:

1. A method for altering the growth characteristics of a plant comprising the step of incorporating into the genome of the plant a recombinant
5 DNA molecule comprising a nucleotide sequence encoding 4-coumarate Co-enzyme A ligase such that when the nucleotide sequence is expressed in the plant, the growth of the plant is altered.
2. The method as set forth in claim 1 wherein the DNA molecule
10 comprises a homologous nucleotide sequence.
3. The method as set forth in claim 1 wherein the DNA molecule comprises a heterologous nucleotide sequence.
- 15 4. The method as set forth in claim 1 wherein the DNA molecule is incorporated into the genome of the plant by transformation using an Agrobacterium transfer vector.
5. The method as set forth in claim 1 wherein the DNA molecule
20 comprises the nucleotide sequence in antisense orientation.
6. The method as set forth in claim 1 wherein the DNA molecule comprises the nucleotide sequence in sense orientation.
- 25 7. The method as set forth in claim 6 wherein the DNA molecule is a cloned cDNA sequence of 4-coumarate Co-enzyme A ligase.
8. The method as set forth in claim 1 wherein the recombinant DNA molecule comprises the promoter sequence of CaMV35S.
- 30 9. The method as set forth in claim 1 wherein said altered growth is manifested as an increase in biomass.

10. A plant having its growth characteristic altered through the incorporation into the genome of the plant a recombinant DNA molecule comprising a nucleotide sequence encoding 4-coumarate Co-enzyme A ligase such that when the nucleotide sequence is expressed in the plant, the growth
5 characteristic of the plant is altered.

11. The plant as set forth in claim 10 wherein the DNA molecule comprises the nucleotide sequence in antisense orientation.

12. The plant as set forth in claim 10 wherein the DNA molecule comprises the nucleotide sequence in sense orientation.

13. The plant as set forth in claim 10 wherein the DNA is incorporated into the genome of the plant by transformation using an
15 Agrobacterium transfer vector.

14. The plant as set forth in claim 10 wherein the DNA molecule is a cloned cDNA sequence encoding 4-coumarate Co-enzyme A ligase.

15. The plant as set forth in claim 10 wherein the DNA molecule comprises the promoter of CaMV35S.

16. The plant as set forth in claim 10 wherein said altered growth is manifested as an increase in plant biomass.

17. The plant as set forth in claim 10 which is a tree.

18. A method for altering a characteristic of a plant comprising the step of genetically down regulating the enzyme 4-coumarate Co-enzyme A
30 ligase, wherein the characteristic is selected from the group consisting of accelerated growth, reduced lignin content, altered lignin structure, increased disease resistance and increased cellulose content.

19. The method of claim 18 wherein the plant is genetically down regulated through incorporation into the genome of the plant a recombinant DNA molecule comprising a nucleotide sequence encoding 4-coumarate Co-enzyme A ligase in antisense orientation.

5

20. The method as set forth in claim 18 wherein the recombinant DNA molecule is incorporated into the genome of the plant by transformation using an Agrobacterium transfer vector.

10

21. The method as set forth in claim 19 wherein the recombinant DNA molecule comprises a homologous nucleotide sequence that is incorporated into the genome of the plant.

15

22. The method as set forth in claim 18 wherein the nucleotide sequence is a cloned cDNA sequence encoding 4-coumarate Co-enzyme A ligase.

20

23. The method as set forth in claim 18 wherein the recombinant DNA molecule comprises a promoter of CaMV35S.

25

24. A plant having a characteristic altered by genetically down regulating the enzyme 4-coumarate Co-enzyme A ligase, wherein the characteristic is selected from the group consisting of accelerated growth, reduced lignin content, altered lignin structure, increased disease resistance and increased cellulose content.

30

25. The plant of claim 24 wherein the plant is genetically down regulated through incorporation into the genome of the plant a recombinant DNA molecule comprising a homologous nucleotide sequence encoding 4-coumarate Co-enzyme A ligase in the antisense orientation.

26. The plant of claim 24 wherein the recombinant DNA molecule is incorporated into the genome of the plant by transformation using an Agrobacterium transfer vector.

5 27. The plant of claim 24 wherein the nucleotide sequence is a cloned cDNA sequence of 4-coumarate Co-enzyme A ligase.

28. The plant of claim 24 wherein the recombinant DNA molecule comprises a promoter of CaMV35S.

10

29. An isolated and purified DNA molecule comprising a DNA segment comprising a transcriptional regulatory region of a plant 4-coumarate Co-enzyme A ligase gene.

15

30. The isolated and purified DNA molecule of claim 29 in which the DNA segment is from aspen.

31. The isolated and purified DNA molecule of claim 29 wherein the DNA segment directs expression of a linked sequence to the xylem of a plant.

20

32. The isolated and purified DNA molecule of claim 29 wherein the DNA segment directs expression of a linked sequence to the epidermal tissue of a plant.

25

33. A method of imparting disease resistance to a plant tissue comprising:

- (a) introducing an expression cassette comprising a recombinant DNA molecule comprising a nucleotide sequence encoding a 4-coumarate Co-enzyme A ligase operably linked to a promoter functional in a plant cell into cells of a plant;
- (b) regenerating said plant cells to provide a transgenic plant; and

30

- (c) expressing the recombinant DNA molecule in the cells of the transgenic plant in an amount effective to render the plant resistant to disease.
- 5 34. The method according to claim 33 wherein the disease is caused by a fungus.
35. The method according to claim 33 wherein the nucleotide sequence is in the antisense orientation.
- 10 36. A transgenic plant prepared by the method of claim 33.
37. A transgenic seed of the transgenic plant of claim 33.
- 15 38. A transgenic plant, which plant is substantially resistant to disease, comprising:
- (a) a native 4-coumarate Co-enzyme A ligase gene, and
- (b) a recombinant DNA molecule comprising a nucleotide sequence encoding 4-coumarate Co-enzyme A ligase operably linked to a promoter functional in a plant wherein the recombinant DNA
- 20 molecule is expressed in an amount effective to confer resistance to the transgenic plant.
39. A method for altering the lignin content in a plant comprising:
- 25 (a) introducing an expression cassette comprising a recombinant DNA molecule encoding a 4-coumarate Co-enzyme A ligase operably linked to a promoter functional in a plant cell into the cells of a plant;
- (b) regenerating said plant cells to provide a transgenic plant; and
- (c) expressing the recombinant DNA molecule in the cells of the
- 30 transgenic plant in an amount effective to alter the lignin content in the plant cells.

40. A transgenic plant having an altered lignin content in the plant cells comprising: a recombinant DNA molecule comprising a nucleotide sequence encoding a plant 4-coumarate Co-enzyme A ligase operably linked to a promoter so that the recombinant DNA molecule is expressed in an amount effective to alter the lignin content of the plant.

41. A method for altering the cellulose content in a plant comprising:

(a) introducing an expression cassette comprising a recombinant DNA molecule comprising a nucleotide sequence encoding a 4-coumarate Co-enzyme A ligase operably linked to a promoter functional in a plant cell into the cells of a plant;

(b) regenerating said plant cells to provide a transgenic plant; and

(c) expressing the recombinant DNA molecule in the cells of the transgenic plant in an amount effective to alter the cellulose content in the plant.

42. A transgenic plant having an altered cellulose content in the plant cells comprising: a recombinant DNA molecule comprising a recombinant DNA molecule sequence encoding a plant 4-coumarate Co-enzyme A ligase operably linked to a promoter so that the recombinant DNA molecule is expressed in an amount effective to alter the cellulose content of the plants.

43. A method for altering the lignin structure in a plant comprising:

(a) introducing an expression cassette comprising a recombinant DNA molecule comprising a recombinant DNA nucleotide sequence encoding a 4-coumarate Co-enzyme A ligase operably linked to a promoter functional in a plant cell into the cells of a plant;

(b) regenerating said plant cells to provide a transgenic plant; and

(c) expressing the recombinant DNA molecule in the cells of the transgenic plant in an amount effective to alter the lignin structure in the plants.

44. A transformed plant having an altered lignin structure comprising: a recombinant DNA molecule comprising a nucleotide sequence encoding a plant 4-coumarate Co-enzyme A ligase operably linked to a promoter so that the

recombinant DNA molecule is expressed in an amount effective to alter the lignin structure of the plant.

45. An expression cassette comprising a transcriptional control region
5 of a 4-coumarate Co-enzyme A ligase gene operably linked to a DNA segment comprising an open reading frame.

46. A method of expressing a DNA segment in the xylem of a plant, comprising:

- 10 (a) introducing an expression cassette comprising a transcriptional control region of a 4-coumarate Co-enzyme A ligase gene operably linked to a DNA segment into cells of a plant;
(b) regenerating the plant cells to provide a transgenic plant; and
(c) expressing the DNA segment in the xylem of a plant.

- 15 47. A method of expressing a DNA segment in the epidermal tissue of a plant, comprising:

- (a) introducing an expression cassette comprising a transcriptional control region of a 4-coumarate Co-enzyme A ligase gene purple
20 operably linked to a DNA segment into cells of a plant;
(b) regenerating the plant cells to provide a transgenic plant; and
(c) expressing the DNA segment in the epidermal tissue of a plant.

48. The method of claim 46 wherein the transgenic plant has altered
25 lignin content, lignin structure, cellulose content or wood quality relative to the corresponding non-transgenic plant.

49. The plant of claim 38 which has altered levels of phenylpropanoids or other secondary metabolites relative to the corresponding
30 non-transgenic plant.

50. The method of claim 1 wherein the plant has enhanced root growth.

51. The plant of claim 10 wherein the plant has enhanced root growth.
52. The method of claim 1 wherein the plant has enhanced root development.
53. The plant of claim 10 wherein the plant has enhanced root development.

SUBSTITUTESHEET (RULE 26)



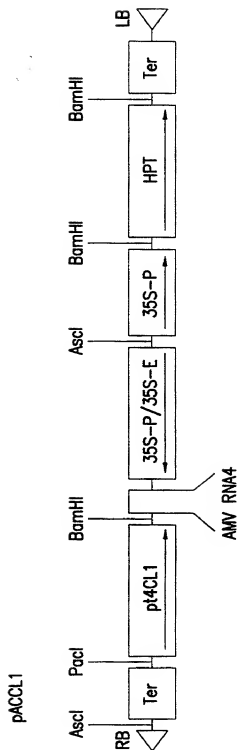


FIG. 2

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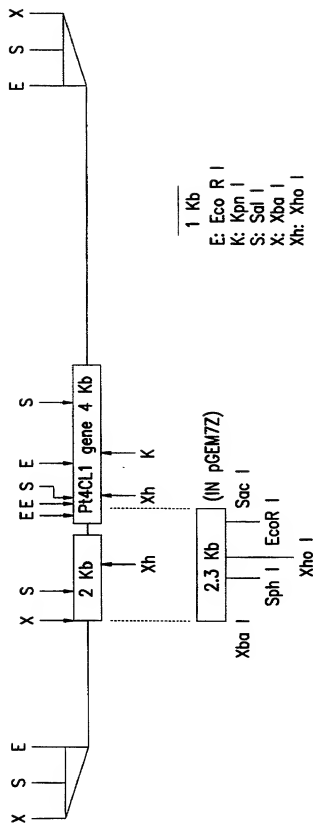


FIG. 3



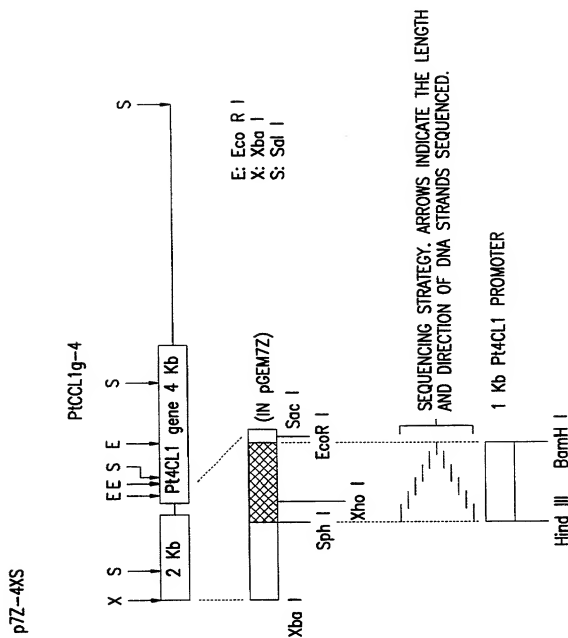
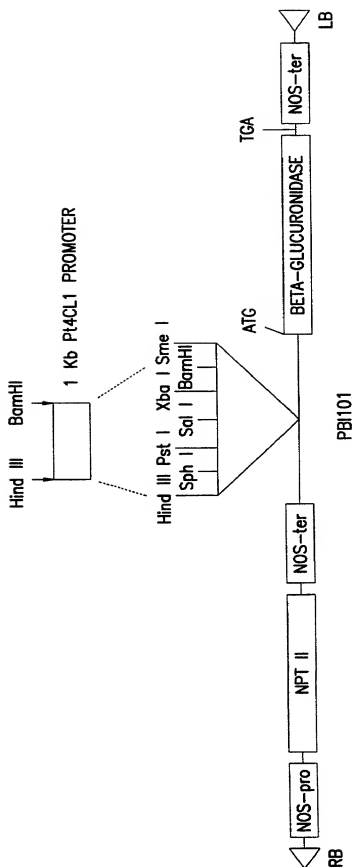


FIG. 5

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Pt4CL1p-GUS



PB101

FIG. 7

2025

Pt4CL2p-GUS

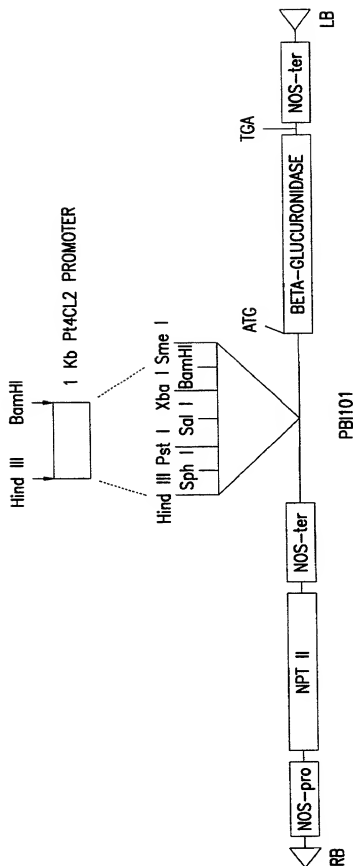


FIG. 8

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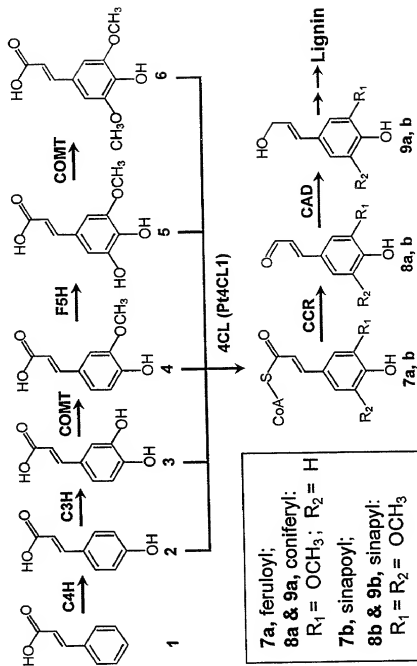


FIG. 9

C 9 3 4 5 6 8

FIG. 10A

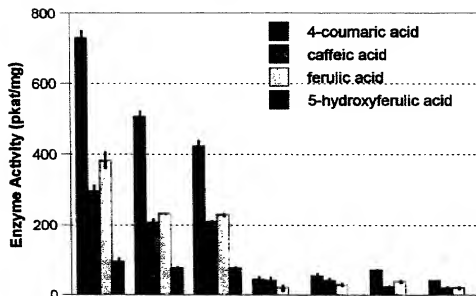


FIG. 10B

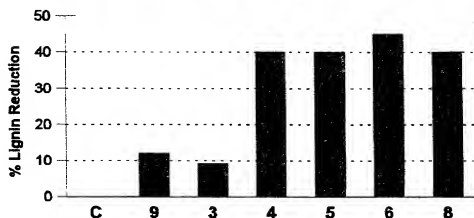


FIG. 10C

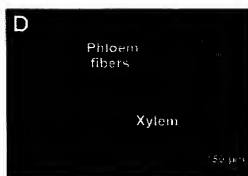


FIG. 10D



FIG. 10E

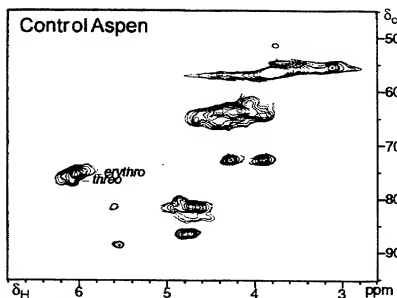


FIG. 11A

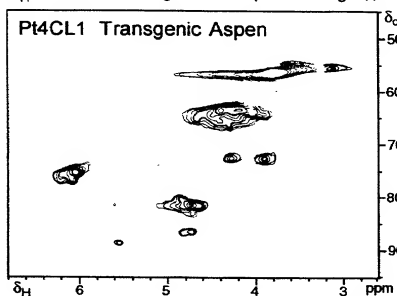


FIG. 11B

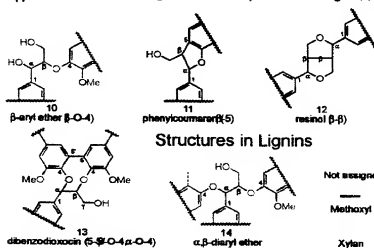
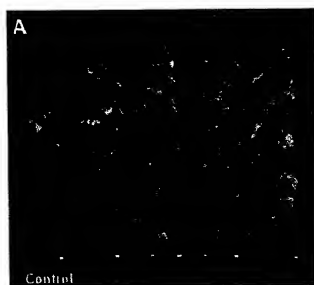
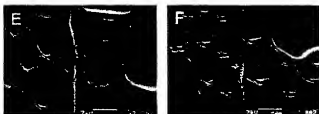
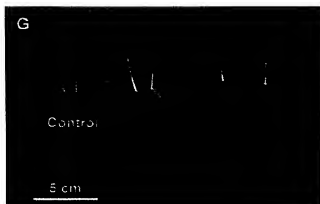


FIG. 11C

**FIG. 12A****FIG. 12B**

**FIG. 12C FIG. 12D****FIG. 12E FIG. 12F****FIG. 12G**

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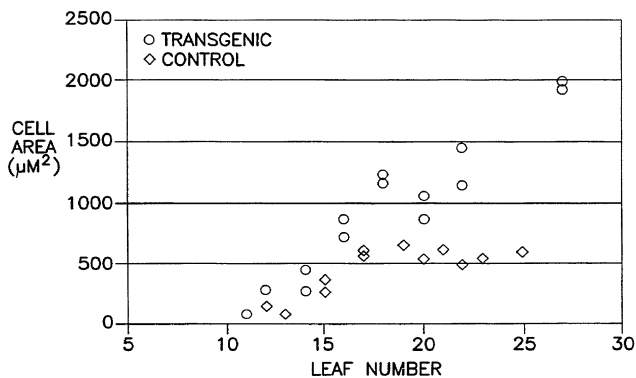


FIG. 12H

Declaration and Power of Attorney For Patent Application

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am an original, first and joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled GENETIC ENGINEERING OF LIGNIN BIOSYNTHESIS IN PLANTS (Attorney Docket No. 66040-9651-01), the specification of which was filed with my authority, on May 3, 2000 as Application Serial No. 09/530,663.

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims referred to above.

I acknowledge the duty to disclose to the Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

And I hereby appoint Joseph A. Gemignani (Reg. No. 19,482), Christopher B. Austin (Reg. No. 41,592), Robert E. Clemency (Reg. No. 19,287), David L. De Bruin (Reg. No. 35,489), Gerald L. Fellows (Reg. No. 36,133), Randall W. Fieldhack (Reg. No. 43,611), Gregory J. Hartwig (Reg. No. P-46,761), Daniel S. Jones (Reg. No. 42,697), Richard L. Kaiser (Reg. No. 46,158), Timothy M. Kelley (Reg. No. 34,201), Casimir F. Laska (Reg. No. 30,862), Edward R. Lawson, Jr. (Reg. No. 41,931), Richard H. Marschall (Reg. No. 39,290), Thomas A. Miller (Reg. No. 36,871), Kevin P. Moran (Reg. No. 37,193), Andrew R. Peret (Reg. No. 41,246), David R. Price (Reg. No. 31,557), Thomas S. Reynolds II (Reg. No. 45,262), David B. Smith (Reg. No. 27,595), Derek C. Stettner (Reg. No. 37,945), Billie Jean Strandt (Reg. No. 36,940), Sheldon L. Wolfe (Reg. No. 43,996), Paul F. Donovan (Reg. No. 39,962), Jill A. Fahrlander (Reg. No. 42,518), Grady J. Frenchick (Reg. No. 29,018), Karen B. King (Reg. No. 41,898), Linda Blair Meier (Reg. No. 39,769), Teresa J. Welch (Reg. No. 33,049), Robert S. Beiser (Reg. No. 28,687), Witold A. Ziarno (Reg. No. 39,888), and each or any of them, my attorneys or agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith.

TO: ADDRESS ALL COMMUNICATIONS IN OR PERTAINING TO THIS APPLICATION

Joseph A. Gemignani
Michael Best & Friedrich LLP
100 East Wisconsin Avenue
Milwaukee, Wisconsin 53202-4108

I hereby claim the benefit under Title 35, United States Code, §120 of the United States applications listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56(a)

which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

Application Serial No.
08/969,046

Filing Date
12 November 1997 ✓

Status
Pending

I hereby claim foreign priority benefits under Title 35, United States Code, §119 of the foreign application for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

PCT/US98/24138 ✓
(Number)

Prior Foreign Application
PCT
(Country)

12 November 1998 ✓
(Day/Month/Year Filed)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

1-00
Full name of first joint inventor: Vincent Lee C. Chiang ✓

Inventor's signature Vincent L. C. Chiang

Date: 7-7-00

Residence:

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Citizenship:

United States of America

Post Office Address:

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Hancock, MI 49930

2-00
Full name of second joint inventor: Chung-Jui Tsai ✓

Inventor's signature Chung-Jui Tsai

Date: 7-6-00

Residence:

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Citizenship:

Taiwan

Post Office Address:

1510 Anthony Street #34
Hancock, MI 49930

Full name of third joint inventor: Wen-Jing Hu

Inventor's signature _____

Date: _____

Residence:

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Citizenship:

Taiwan

Post Office Address:

8299 Cambridge Drive #1003
Houston, TX 77054

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Michael Best & Friedrich LLP
100 East Wisconsin Avenue
Milwaukee, Wisconsin 53202-4108

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Full name of first joint inventor: Vincent Lee C. Chiang

Inventor's signature _____
Date: _____
Residence: Hancock, Michigan
Citizenship: United States of America
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Hancock, MI 49930

Full name of second joint inventor: Chung-Jui Tsai

Inventor's signature _____
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Citizenship: Taiwan
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3-10 Full name of third joint inventor: Wen-Jing Hu

Inventor's signature Wen-Jing Hu
Date: 7/6/2000
Residence: Houston, Texas
Citizenship: Taiwan
Post Office Address: 8299 Cambridge Drive #1003
Houston, TX 77054

SEQUENCE LISTING

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001120-23992923

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 Cys Tyr Tyr Glu Lys Val Lys Asp Phe Ala Arg Glu Ser Asp Val Lys
 130 135 140
 Val Met Cys Val Asp Ser Ala Pro Asp Gly Ala Ser Leu Phe Arg Ala
 145 150 155
 His Thr Gln Ala Asp Glu Asn Glu Val Pro Gln Val Asp Ile Ser Pro
 165 170 175
 Asp Asp Val Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro
 180 185 190
 Lys Gly Val Met Leu Thr His Lys Gly Leu Ile Thr Ser Val Ala Gln
 195 200 205
 Gln Val Asp Gly Asp Asn Pro Asn Leu Tyr Phe His Ser Glu Asp Val
 210 215 220
 Ile Leu Cys Val Leu Pro Met Phe His Ile Tyr Ala Leu Asn Ser Met
 225 230 235
 Met Leu Cys Gly Leu Arg Val Gly Ala Ser Ile Leu Ile Met Pro Lys
 245 250 255
 Phe Glu Ile Gly Ser Leu Leu Gly Leu Ile Glu Lys Tyr Lys Val Ser
 260 265 270
 Ile Ala Pro Val Val Pro Pro Val Met Met Ala Ile Ala Lys Ser Pro
 275 280 285
 Asp Leu Asp Lys His Asp Leu Ser Ser Leu Arg Met Ile Lys Ser Gly
 290 295 300
 Gly Ala Pro Leu Gly Lys Glu Leu Glu Asp Thr Val Arg Ala Lys Phe
 305 310 315
 Pro Gln Ala Arg Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro
 325 330 335
 Val Leu Ala Met Cys Leu Ala Phe Ala Lys Glu Pro Phe Asp Ile Lys
 340 345 350
 Pro Gly Ala Cys Gly Thr Val Val Arg Asn Ala Glu Met Lys Ile Val
 355 360 365
 Asp Pro Glu Thr Gly Val Ser Leu Pro Arg Asn Gln Pro Gly Glu Ile
 370 375 380
 Cys Ile Arg Gly Asp Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro Glu
 385 390 395
 Ala Thr Ser Arg Thr Ile Asp Lys Glu Gly Trp Leu His Thr Gly Asp
 405 410 415
 Ile Gly Tyr Ile Asp Asp Asp Asp Glu Leu Phe Ile Val Asp Arg Leu
 420 425 430
 Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Thr Glu Leu
 435 440 445
 Glu Ala Leu Leu Ile Ala His Pro Glu Ile Ser Asp Ala Ala Val Val
 450 455 460
 Gly Leu Lys Asp Glu Asp Ala Gly Glu Val Pro Val Ala Phe Val Val
 465 470 475
 Lys Ser Glu Lys Ser Gln Ala Thr Glu Asp Glu Ile Lys Gln Tyr Ile
 485 490 495
 Ser Lys Gln Val Ile Phe Tyr Lys Arg Ile Lys Arg Val Phe Phe Ile
 500 505 510
 Glu Ala Ile Pro Lys Ala Pro Ser Gly Lys Ile Leu Arg Lys Asn Leu

515 520 525
 Lys Glu Lys Leu Pro Gly Ile
 530 535

<210> 3
 <211> 1710
 <212> DNA
 <213> Populus tremuloides Michx. (aspen)

<220>
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 <222> (1)...(1710)

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 cca caa aac caa aac gca cca tcc tct cat gaa act gat cac att ttc 96
 Pro Gln Asn Gln Asn Ala Pro Ser Ser His Glu Thr Asp His Ile Phe
 20 25 30
 aga tca aaa cta cca gac ata acc atc tcg aac gac ctc cct ctg cac 144
 Arg Ser Lys Leu Pro Asp Ile Thr Ile Ser Asn Asp Leu Pro Leu His
 35 40 45
 gca tac tgc ttt gaa aac ctc tct gat ttc tca gat agg cca tgc ttg 192
 Ala Tyr Cys Phe Glu Asn Leu Ser Asp Phe Ser Asp Arg Pro Cys Leu
 50 55 60
 att tca ggt tcc acg gga aaa acc tat tct ttt gcc gaa act cac ctc 240
 Ile Ser Gly Ser Thr Gly Lys Thr Tyr Ser Phe Ala Glu Thr His Leu
 65 70 75 80
 ata tct cgg aag gtc gct gct ggg tta tcc aat ttg ggc atc aag aaa 288
 Ile Ser Arg Lys Val Ala Ala Gly Leu Ser Asn Leu Gly Ile Lys Lys
 85 90 95
 ggc gat gta atc atg acc ctg ctc caa aac tgc cca gaa ttc gtc ttc 336
 Gly Asp Val Ile Met Thr Leu Leu Gln Asn Cys Pro Glu Phe Val Phe
 100 105 110
 tcc ttc atc ggt gct tcc atg att ggt gca gtc atc acc act gcg aac 384
 Ser Phe Ile Gly Ala Ser Met Ile Gly Ala Val Ile Thr Thr Ala Asn
 115 120 125
 cct ttc tac act caa agt gaa ata ttc aag caa ttc tct gct tct cgt 432
 Pro Phe Tyr Thr Gln Ser Glu Ile Phe Lys Gln Phe Ser Ala Ser Arg
 130 135 140
 gcg aaa ctg att atc acc cag tct caa tat gtg aac aag cta gga gat 480
 Ala Lys Leu Ile Ile Thr Gln Ser Gln Tyr Val Asn Lys Leu Gly Asp
 145 150 155 160
 agt gat tgc cat gaa aac aac caa aaa ccg ggg gaa gat ttc ata gta 528
 Ser Asp Cys His Glu Asn Asn Gln Lys Pro Gly Glu Asp Phe Ile Val
 165 170 175
 atc acc att gat gac ccg cca gag aac tgt cta cat ttc aat gtg ctt 576
 Ile Thr Ile Asp Asp Pro Pro Glu Asn Cys Leu His Phe Asn Val Leu

| 180 | 185 | 190 | |
|---|-----|-----|------|
| gtc gag gct agc gag agt gaa atg cca aca gtt tca atc ctt ccg gat Val Glu Ala Ser Glu Ser Glu Met Pro Thr Val Ser Ile Leu Pro Asp 195 200 205 | | | 624 |
| gat cct gtg gca tta cca ttc tct tca ggg aca aca ggg ctc cca aaa Asp Pro Val Ala Leu Pro Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys 210 215 220 | | | 672 |
| gga gtg ata ctg acc cac aag agc ttg ata aca agt gtg gct caa caa Gly Val Ile Leu Thr His Lys Ser Leu Ile Thr Ser Val Ala Gln Gln 225 230 235 240 | | | 720 |
| gtt gat gga gag atc cca aat tta tac ttg aaa caa gat gac gtt gtt Val Asp Gly Glu Ile Pro Asn Leu Tyr Leu Lys Gln Asp Asp Val Val 245 250 255 | | | 768 |
| tta tgc gtt tta cct ttg ttt cac atc ttt tca ttg aac agc gtg ttg Leu Cys Val Leu Leu Pro Leu Phe His Ile Phe Ser Leu Asn Ser Val Leu 260 265 270 | | | 816 |
| tta tgc tgc ttg aga gcc ggt tct gct gtt ctt tta atg caa aag ttt Leu Cys Ser Leu Arg Ala Gly Ser Ala Val Leu Leu Met Gln Lys Phe 275 280 285 | | | 864 |
| gag ata gga tca ctg cta gag ctc att cag aaa cac aat gtt tgc gtt Glu Ile Gly Ser Leu Leu Glu Leu Ile Gln Lys His Asn Val Ser Val 290 295 300 | | | 912 |
| gcg gct gtg gtg cca cca ctg gtg ctg gcg ttg gcc aag aac cca ttg Ala Ala Val Val Pro Pro Leu Val Leu Ala Leu Ala Lys Asn Pro Leu 305 310 315 320 | | | 960 |
| gag gcg aac ttc gac ttg agt tgc atc agg gta gtc ctg tca ggg gct Glu Ala Asn Phe Asp Leu Ser Ser Ile Arg Val Val Leu Ser Gly Ala 325 330 335 | | | 1008 |
| gcg cca ctg ggg aag gag ctc gag gac gcc ctc agg agc agg gtt cct Ala Pro Leu Gly Lys Glu Leu Glu Asp Ala Leu Arg Ser Arg Val Pro 340 345 350 | | | 1056 |
| caq gcc atc ctg gga cag ggt tat ggg atg aca gag gcc ggg cct gtg Gln Ala Ile Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val 355 360 365 | | | 1104 |
| cta tca atg tgc tta gcc ttt tca aag caa cct ttc cca acc aag tct Leu Ser Met Cys Leu Ala Phe Ser Lys Gln Pro Phe Pro Thr Lys Ser 370 375 380 | | | 1152 |
| ggg tgc tgt gga acg gtg gtt aga aac gca gag ctc aag gtc att gac Gly Ser Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Ile Asp 385 390 395 400 | | | 1200 |
| cct gag acc ggt cgc tct ctt ggt tac aac caa cct ggt gaa atc tgc Pro Glu Thr Gly Arg Ser Leu Gly Tyr Asn Gln Pro Gly Glu Ile Cys 405 410 415 | | | 1248 |
| atc cgt gga tcc caa atc atg aaa gga tat ttg aat gac gcg gaa gcc Ile Arg Gly Ser Gln Ile Met Lys Gly Tyr Leu Asn Asp Ala Glu Ala 420 425 430 | | | 1296 |

7

acg gca aac acc ata gac gtt gag ggt tgg ctc cac act gga gat ata 1344
 Thr Ala Asn Thr Ile Asp Val Glu Gly Trp Leu His Thr Gly Asp Ile
 435 440 445

ggt tat gtc gac gac gac gac gag att ttc att gtt gat aga gtg aag 1392
 Gly Tyr Val Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Val Lys
 450 455 460

gaa atc ata aaa ttc aaa ggc ttc cag gtg ccg cca gcg gag ctt gag 1440
 Glu Ile Ile Lys Phe Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu
 465 470 475 480

gct ctc ctt gta aac cac cct tca att gcg gat gcg gct gtt gtt ccg 1488
 Ala Leu Leu Val Asn His Pro Ser Ile Ala Asp Ala Ala Val Val Pro
 485 490 495

caa aaa gac gag gtt gct ggt gaa gtt cct gtc gcg ttt gtg gtc cgc 1536
 Gln Lys Asp Glu Val Ala Gly Glu Val Pro Val Ala Phe Val Val Arg
 500 505 510

tca gat gat ctt gac ctt agt gaa gag gct gta aaa gaa tac att gca 1584
 Ser Asp Asp Leu Asp Leu Ser Glu Glu Ala Val Lys Glu Tyr Ile Ala
 515 520 525

aag cag gtg gtg ttc tac aag aaa ctg cac aag gtg ttc ttc gtt cat 1632
 Lys Gln Val Val Phe Tyr Lys Lys Leu His Lys Val Phe Phe Val His
 530 535 540

tct att ccc aaa tcg gct tct gga aag att cta aga aaa gac ctc aga 1680
 Ser Ile Pro Lys Ser Ala Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg
 545 550 555 560

gcc aag ctt gcc aca gcc acc acc atg tcc 1710
 Ala Lys Leu Ala Thr Ala Thr Met Ser
 565 570

<210> 4
 <211> 570
 <212> PRT
 <213> Populus tremuloides Michx. (aspen)

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 Pro Gln Asn Gln Asn Ala Pro Ser Ser His Glu Thr Asp His Ile Phe
 20 25 30
 Arg Ser Lys Leu Pro Asp Ile Thr Ile Ser Asn Asp Leu Pro Leu His
 35 40 45
 Ala Tyr Cys Phe Glu Asn Leu Ser Asp Phe Ser Asp Arg Pro Cys Leu
 50 55 60
 Ile Ser Gly Ser Thr Gly Lys Thr Tyr Ser Phe Ala Glu Thr His Leu
 65 70 75 80
 Ile Ser Arg Lys Val Ala Ala Gly Leu Ser Asn Leu Gly Ile Lys Lys
 85 90 95
 Gly Asp Val Ile Met Thr Leu Leu Gln Asn Cys Pro Glu Phe Val Phe
 100 105 110
 Ser Phe Ile Gly Ala Ser Met Ile Gly Ala Val Ile Thr Thr Ala Asn
 115 120 125
 Pro Phe Tyr Thr Gln Ser Glu Ile Phe Lys Gln Phe Ser Ala Ser Arg

130 135 140
 Ala Lys Leu Ile Ile Thr Gln Ser Gln Tyr Val Asn Lys Leu Gly Asp
 145 150 155 160
 Ser Asp Cys His Glu Asn Asn Gln Lys Pro Gly Glu Asp Phe Ile Val
 165 170 175
 Ile Thr Ile Asp Asp Pro Pro Glu Asn Cys Leu His Phe Asn Val Leu
 180 185 190
 Val Glu Ala Ser Glu Ser Glu Met Pro Thr Val Ser Ile Leu Pro Asp
 195 200 205
 Asp Pro Val Ala Leu Pro Phe Ser Ser Gly Thr Thr Gly Leu Pro Lys
 210 215 220
 Gly Val Ile Leu Thr His Lys Ser Leu Ile Thr Ser Val Ala Gln Gln
 225 230 235 240
 Val Asp Gly Glu Ile Pro Asn Leu Tyr Leu Lys Gln Asp Asp Val Val
 245 250 255
 Leu Cys Val Leu Pro Leu Phe His Ile Phe Ser Leu Asn Ser Val Leu
 260 265 270
 Leu Cys Ser Leu Arg Ala Gly Ser Ala Val Leu Leu Met Gln Lys Phe
 275 280 285
 Glu Ile Gly Ser Leu Leu Glu Leu Ile Gln Lys His Asn Val Ser Val
 290 295 300
 Ala Ala Val Val Pro Pro Leu Val Leu Ala Leu Ala Lys Asn Pro Leu
 305 310 315 320
 Glu Ala Asn Phe Asp Leu Ser Ser Ile Arg Val Val Leu Ser Gly Ala
 325 330 335
 Ala Pro Leu Gly Lys Glu Leu Glu Asp Ala Leu Arg Ser Arg Val Pro
 340 345 350
 Gln Ala Ile Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val
 355 360 365
 Leu Ser Met Cys Leu Ala Phe Ser Lys Gln Pro Phe Pro Thr Lys Ser
 370 375 380
 Gly Ser Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Ile Asp
 385 390 395 400
 Pro Glu Thr Gly Arg Ser Leu Gly Tyr Asn Gln Pro Gly Glu Ile Cys
 405 410 415
 Ile Arg Gly Ser Gln Ile Met Lys Gly Tyr Leu Asn Asp Ala Glu Ala
 420 425 430
 Thr Ala Asn Thr Ile Asp Val Glu Gly Trp Leu His Thr Gly Asp Ile
 435 440 445
 Gly Tyr Val Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Val Lys
 450 455 460
 Glu Ile Ile Lys Phe Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu
 465 470 475 480
 Ala Leu Leu Val Asn His Pro Ser Ile Ala Asp Ala Ala Val Val Pro
 485 490 495
 Gln Lys Asp Glu Val Ala Gly Glu Val Pro Val Ala Phe Val Val Arg
 500 505 510
 Ser Asp Asp Leu Asp Leu Ser Glu Glu Ala Val Lys Glu Tyr Ile Ala
 515 520 525
 Lys Gln Val Val Phe Tyr Lys Lys Leu His Lys Val Phe Phe Val His
 530 535 540
 Ser Ile Pro Lys Ser Ala Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg
 545 550 555 560
 Ala Lys Leu Ala Thr Ala Thr Thr Met Ser
 565 570

<210> 5

<211> 1172

<212> DNA

<213> Populus tremuloides Michx. (aspen)

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 atggctatga tgaaggttaa tagaggtagt tgtgatygag atatgtccag cactagtttt 180
 ttgtgtggtg gattctccat gatgacggga aaattttaca tatatatata atgaataata 240
 tgaatgattt ttctctgtaa ttgtgtgaaa tagatttaaa cagctcaatg tgaagtgacc 300
 agttgtcaca tgaccactcg acttggggca tgggtgattt tcaaatcaca actcaattg 360
 aaaaactaaa ttaaaaaaga tttagattat taaattatta ggttaattca cgggttggt 420
 aatcaattat tattaattaa aacgctagta tttttgataa tttaattaaa attttattgg 480
 atttgaatga actcaattac atcaaaaaa acctaatcaa attaattatc tatgtgatat 540
 aattagaana tataaatgat taacctttaa atctcgagt tctctattaa aaaacacgta 600
 taattgggct agatttaaca gctattatc aaactggcca ggacaattat taaaattaat 660
 aattattatt ttttttaata aagcacttcc taattgttaa aatatatgtc taaacacata 720
 taataaaatt tattttgtga tctttggcag taggtgagag gtgctgacaa ataaattagt 780
 gcataaaaaa taatggattg gtggtctgtg aaaagacagg tggaggacaa gccacctctc 840
 tcaagtcaaa aggcatttcc acaaccaacc caaatgggaa cccaccaccg ttccccgcc 900
 taaaaatccc taatctcacc aaccaaacct cacagattct tcaccaaagc caactgatt 960
 ttcaatcaat gttttcccta tactaccccc ccaacaactc cataataacc aattgttctc 1020
 ttcaccaacc cccgtctctc gtgcagcca attctatctc agcaggaaat cctctgactc 1080
 tgctttctca ggtctctcac cataagaaaa cagagagcac ctaaaactgc ccattctctc 1140
 ctcgtcatct ttgcccgcga atggacgcga ca 1172

<210> 6

<211> 1180

<212> DNA

<213> *Populus tremuloides* Michx. (aspen)

<400> 6

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 tatattttta aaaaattaaa aattaaatta taacattttt attttatccc tcaattacta 180
 aaatgaggtt ggtaataaga attcatgaag ggagttatat atcaaatgat attagttaag 240
 ctattttgat atttataccc taactattac ttatggaata aaaaatttag attattataa 300
 aatattttat ggatttcagg tattcatatg aatatttatt tgattattat ttattcaaca 360
 aaaaataaaa caattaatat gcatgtttga agttttatata tatattaagt taggtttaga 420
 tagattttgg gtggggttaa ttaattatca taccctatct actatctatc aaataatcca 480
 aataaattca cctaataatg gttgggtttg tattcatcaa gtttaacatta aattgtaat 540
 ccgtaagtga ctaaacaaagt acaaaagact ctattttatc ctatatatta ccataaagoc 600
 aactataatt cctattcttt ttcatccctt ctatcgtaat ttctctgtgac ttltttattt 660
 atatatatac ggtaacgaaa cacagcaata aaagtatttg tgaagatat ggataattat 720
 tatggtgact atgaagagat aaatttgcca tgacataagt tctcagtgtc atctcataaa 780
 agactgtctt gccacgtaaq ctgtgtgag gtgtcgtttt ttacgctgtg caaccaatcg 840
 ctgcgaattg actctttgag gtaggtgaga gcttcggctt tgatgggaac gcatgaggc 900
 atagggtttg gttctttgaa tgtgagatag gcatgctttg gctcccttgc tactcacctc 960
 atcttcaatt tgccagctca gctaccagtc tctcaccact agtttcacca aaatttctct 1020
 gctcctgtat ttattacacc ttgctcgatt ggctccgtct tctgtacacg atccacacgg 1080
 atcgatcgat tagaaccata cagaattggg attggttggg ttatcattct gogttagata 1140
 catctatcac agaagaaac tcccttccat ctacggaaac 1180

<210> 7

<211> 12

<212> PRT

<213> *Populus tremuloides* Michx. (aspen)

<400> 7

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<210> 8

<211> 7

10

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<212> PRT
<213> Populus tremuloides Michx. (aspen)

<400> 8
Gly Glu Ile Cys Ile Arg Gly
1           5

<210> 9
<211> 31
<212> DNA
<213> Populus tremuloides Michx. (aspen)

<400> 9
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<210> 10
<211> 28
<212> DNA
<213> Populus tremuloides Michx. (aspen)

<400> 10
ttggatccgt igcicarcar gtigaygg 28

<210> 11
<211> 27
<212> DNA
<213> Populus tremuloides Michx. (aspen)

<400> 11
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<210> 12
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<212> PRT
<213> Populus tremuloides Michx. (aspen) unknown

<400> 12
Gly Glu Ile Cys Ile Arg Gly
1           5

<210> 13
<211> 27
<212> DNA
<213> Populus tremuloides Michx. (aspen)

<400> 13
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<210> 14
<211> 26
<212> DNA
<213> Populus tremuloides Michx. (aspen)

<400> 14
ttagatctct aggacatggt ggtggc 26

<210> 15
<211> 16
<212> DNA
<213> Populus tremuloides Michx. (aspen)

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      <210> 16
      <211> 6
      <212> DNA
      <213> Populus tremuloides Michx. (aspen)

      <400> 16
ccggttc
      <210> 17
      <211> 11
      <212> DNA
      <213> Populus tremuloides Michx. (aspen)

      <400> 17
tctcaccaac c

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